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Name=2;
IsoId=Q9UKR0-2; Sequence=VSP 005403;
-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Secreted (Probable).
-!- ALTERNATUS PRODUCTS:
- Event=Alternative splicing; Named isoforms=2;
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IsoId=Q9UKR0-1; Sequence=Displayed;
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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KYVDWIRMIRNN -> NSTLVGLGTSWNFNSCQPF (in
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR0010254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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R PRINTS; PR00722; CHYMOTRYPSIN.
R PROSTIE; PS00240; TRYPSIN DOM; 1.
R PROSTIE; PS00134; TRYPSIN DOM; 1.
R PROSTIE; PS00135; TRYPSIN JES; 1.
R PROSTIE; PS00135; TRYPSIN JES; 1.
R PAGINES; Serine protease; Glycoprotein; Signal; Alternative splicing.
SIGNAL 1.
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EMBL, PRT35025, AAF06651.1; --
EMBL, AF24527; AAG33365.1; --
EMBL, AC011473; AAG33258.1; --
EMSP, POOT63; LDPO.
MESP, SOUT63; LDPO.
MESPS, SOL. 020; --
Genew, HGNC: 6360; KLK12.
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SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffeld J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,

Arellano A., Sanders C., Ow D., Nolam M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;

Sequence analysis of chromosome 19q13.4.",

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Suggested to be involved in kindling epileptogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of tumor-associated differentially expressed gene-14, a novel serine protease overexpressed by ovarian carcinoma."; Cancer Res. 59:4435-4439(1999).
TLKE HUMAN STANDARD; PRT; 260 AA.

760252, Q9HCBA; Q9UQ47;

15-UTL-1999 (Rel. 38, Last sequence update)

15-UTL-2099 (Rel. 43, Last annotation update)

15-WAR-2004 (Rel. 43, Last annotation update)

Neuropsin precursor (RC 3 4 21.-) ((RP) (Kallikrein 8) (Ovasin) (Serine protesse TADG-14) (Tumor-associated differentially expressed gene-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.; "A novel form of human neuropsin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain.";
                                                                                                                                                                                                                                                                                                                                                               Yoshida S., Taniguchi M., Hirata A., Shiosaka S.; "Sequence analysis and expression of human neuropsin cDNA and gene."; Gene 213:9-16(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOPORM 1).

Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;

"Molecular closhing and characterization of a novel serine protease,
ovasin, a potential molecular marker for ovarian carcinomas.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99413504; PubMed=10485494;
Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
                                                                                                                                                                                                                     Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J. Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19913 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hippocampal plasticity.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.-|- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATUE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 260:627-634(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20510030; PubMed=11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99203457, PubMed=10102990;
                                                                                                                                                                                                                                                                                                                               IISSUE=Hippocampus;
MEDLINE=98372070; PubMed=9714609;
                                                                                                                                                                            KLK8 OR PRSS19 OR TADG14 OR NRPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 257:119-130(2000).
                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Ovary;
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                          protein).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE SECOND II; TISSUE=Mammary gland;

Klausner R.D., Feingold E.14.7932,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh R.K.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Kapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Scheorgren E.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rocherth A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

Human and mouse colMs sequences.",
                                                                                                                                              TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKXVDW 240
                               121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
                                                                                   GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI 192
                                                                                                                                                                                                      TDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and assignment of mouse neuropsin gene, Prss19 to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c, TISSUE-Hippocampus;
MEDLINE=95348817; PubMed=7623137;
Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
Ito C., Mishino H., Aimoto S., Kiyama H., Shiosaka S.;
"Expression and activity-dependent changes of a novel limbic-serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last sequence update)
15-JRR-2004 (Rel. 43, Last annotation update)
Neuropsin precursor (BC 3.4.21.-) (NP) (Kallikrein
KLK8 OR PRSS19 OR NRPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hirata A., Inoue N., Shiosaka S.;
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STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=98225202; PubMed=9556608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procease gene in the hippocampus.";
J. Neurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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IKXII 256
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Q61955;
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                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                 Isold=O60259-2; Sequence=VSP 005401;
TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the pancreas while isoform 2 is expressed in adult brain and hippocampus. Both forms are also found in fetal brain and placenta. Not detected in kidney, spleen, liver and lung. SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 IFLLL---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWYLTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAM; PF00089; LTYPSin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
PRART; SM0020; LTYP_SPC. 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN BIS; 1.
Hydrolaes; Serine protease; Glycoprotein; Zymogen; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WRSNPLPPAA (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 605644; -.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
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IsoId=060259-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0007399; P:neurogenesis; TAS.
InterPro; IPR009003; Cys. Ser trypsin.
InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB009849; BAA28673.1; --
BMBL, AB012761; BAA2876.1; --
EMBL, AB010780; BAA8684.1; --
EMBL, AB008390; BAA82665.1; --
EMBL, AB008927; BAA82666.1; --
EMBL, AF055982; AAD56050.1; --
EMBL, AF055942; AAD25979.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF095743; AAD29574.1; -. AF243527; AAG33361.1; -. AC011473; AAG23254.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.244; -.
Genew; HGNC:6369; KLK8.
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184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               TISSUE-Hippocampus;
MEDLINE-99134351; PubMed=9933620;
MEDLINE-99134351; PubMed=9933620;
Mishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
Shiosaka S., Hakoshima T.;
"Crystal structure of neuropsin, a hippocampal protease involved in
kindling epileptogenesis.";
J. Biol. Chem. 274:4220-4224(1999).
J. Biol. Chem. 274:4220-4224(1999).
J. PUNCTION: Suggested to be involved in kindling epileptogenesis and
hippocampal plasticity. Has a strong proteolytic activity against
                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Expressed specifically in the limbic system of mouse brain and is localized at highest concentration in pyramidal neurons of the hippocampal CAL-3 subfields.

-i- MASS SPECTROMETRY: NW=26613; METHOD=MALDI; RANGE=29-260.

-i- MASS SPECTROMETRY: NW=26229; METHOD=MALDI; RANGE=33-260.

-i- SIMILARITY: Belongs to peptidase family SI. Kallikrein subfamily.
                                                                                                                                                                                                                                                               fibronectin.
CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by dIIsopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase, Serine protease, Glycoprotein, Zymogen, Signal, 3D-structure.
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EMBL; AB032202; BAA92435.1; -.
EMBL; 156559; 156559.
PIR; 156559; 156559.
PDB; INPW; 23-MAR-99.
MREOPS; S01.244; -.
MGD; MGI:892018; KIR8.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
Pfam; PP00089; trypsin; 1.
PRNNTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SFC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
    plasticity-related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRVPVRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFILICV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.3%; Score 622.5; DB 1; Length 260; 49.0%; Pred. No. 5.1e-44; ive 28; Mismatches 93; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                         28523 MW; BESF6F6BE37CD60E CRC64;
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Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.0%
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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254 KTM 256
                                                              HUMAN
                                               RESULT 5
                                                               KLKB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 NMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRVTS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 KVKPIELANLCPKVGQKCIISGWGTVTSPQENPPNTLNCAEVKIYSQNKCERAYPGKITE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 GMYCAGSSNGADICQGDSGGPLVCNGVLQGITIMGS-DPCGKPEKPGVYIKICRYINWIK 253
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                            MEDILINE=98389725; PubMed=972524;
MEDILINE=98389725; PubMed=972524;
MEDILINE=98389725; PubMed=972524;
MEDILINE=98389725; PubMed=972524;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
J. Biol. Chem. 273:23004-23011(1998).";
J. Biol. Chem. 273:23004-23011(1998).";
J. PUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against fibronectin (By similarity).
J. CATALYTIC ACTIVITY: Preferential cleavage: Arg., Lys...
J. SUBCELIGILAR LOCATION: Secreted (By similarity).
J. TISSUE SPECIFICITY: Restricted to hippocampus.
J. SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 IFLLL-CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHC
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS00130; TRYPSIN LDOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ005641; CAA06643.1; -.
HSSP; Q61955; 1NPM.
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260 AA;
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   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.244;
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SEQUENCE FROM N.A. (ISOFORM 1).

Lamerdin J.B., McCready P.M., Skowronski B., Viswanathan V.,

Lamerdin J.B., McCready P.M., Skowronski B., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=2288257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z
                                                                                                                                                                                                                                                                                                                                                                Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S., "cDNA cloning and expression of a novel serine protease, TLSP.";
Biochim. Biophys. Acta 1399:225-228(1998).
KLKB_HUMAN STANDARD; PRT; 250 AA.

$\text{PUMAN}$ O9NS65;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Hippocampus, and Prostate;
MEDLINE=20329229; PubMed=10872828;
MEDLINE=20329229; PubMed=10872828;
MISTSI S., Yamada T., Okul A., Kominami K., Uemura H., Yamaguchi I and Isoform of a kallikrein-like protease, TLSP/hippostasin, (PRSS20), is expressed in the human brain and prostate.";
Biochem. Biophys. Res. Commun. 272:205-211(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20510030; PubMed=11054554; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.;
                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20130117; PubMed=10662548;
Yousef G.M., Scorilas A., Diamandis E.P.;
Genomic organization, mapping, tissue expression, and hor regulation of trypsin-like serine protease (TLSP PRSS20), member of the human kallikrein gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                        TISSUE-Hippocampus;
MEDLINE-98438738; PubMed-9765601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                               KLK11 OR PRSS20 OR TLSP.
                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Schwutz J., Myers R.W., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNR sequences."; "Froc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

-!- FUNCTION: Possible multifunctional protease. Efficiently cleaves bz-phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and weakly cleaves other substrates for kallikrein and trypsin.

-!- SUBCELULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate. Isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=Q9UBX7-2; Sequence=VSP 005402;
TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform
1 is expressed preferentially in brain; isoform 2 in prostate.
SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-NORLEWINDWKSSGRGITAAKEPGARSEPLOAM
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N-LINKED (GLCNAC. ..) (F
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GO; GO:0008236; F:serine-type peptidase activity; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               lsoId=09UBX7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB012917; BAA33404.1; ALT_INIT.
EMBL; AB013730; BAA88713.1; --
EMBL; AB041036; BAA98773.1; --
EMBL; AF164623; AA047815.1; --
EMBL; AF243527; AA047815.1; --
EMBL; AF243527; AA033364.1; --
EMBL; BC012408; AA047815.1; --
EMBL; BC022068; AA0478063; --
HSSP; P00763; --
HSSP; P00763; --
EMBL; --
EMB
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Interpro; IPR001254; Peptidase_S1.
Interpro; IPR001314; Peptidase_S1A.
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"A novel serine proteinase-like sequence from human brain.";
Biochim. Biophys. Acta 1218:225-228(1994).
-!- FUNCTION: Protease whose physiological substrate is not yet known.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                 3 LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                    4 LOLILLALATGLVGGET-RIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
                                                                                                                                                                                                                                               121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P., "Molecular cloning of the human kallikrein 15 gene (KLKL5). Upregulation in prostate cancer.";
J. Biol. Chem. 276:53-61(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY Pubmed=11010966;
                                                                                         5
                                                             Length 250;
                                                                                           Indels
             /FTId=VSP 005402.
250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09HZR5; QL5358; Q9HZR3; Q9HZR4; Q9HZR6; Q9HBG9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=4;
                                                                                           89;
                                                             DB 1;
                                                             Score 618.5; DB Pred. No. 1e-43;
                                                  45.0%; Scott No. 1c.
48.2%; Pred. No. 1c.
1've 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AA
(in isoform 2)
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IsoId=Q9H2R5-2; Sequence=VSP_005405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY PARTIAL SEQUENCE FROM N.A.
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MEDLINE=20510030; PubMed=11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=94289486; PubMed=8018728;
                                                                                            Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                             Query Match
Best Local Similarity
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                                   SEQUENCE
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DR EMEL, UIS157; AAA79941.1; -.

DR EMEL, UIS157; AAA79941.1; -.

DR HENORS; DRO0163; IDDO.

DR HENORS; PRO01763; IDDO.

DR HENORS; PRO01763; IDDO.

DR PRINTS; PRO01764; Peptidase_SID.

DR PRINTS; PRO01764; Peptidase_SID.

DR PROSTITE; PRO01767; TYPESIN DAY; IDDR.

DR PROSTITE; PRO01767; TRYPESIN DAY; IDDR.

DR PROSTITE; PRO01767; TRYPESIN DAY; IDDR.

DR PROSTITE; PRO01767; TRYPESIN DAY; IDDR.

RW HYDOOLAGE; PROFESIN DAY; IDDR.

CALCIUM-Dinding; Signal; Multigene family.

TO ACTIVATION PEPTING BY SIMILARITY).

TO CALCIUM (VIA CARBONIL OXYGEN)

CALCIUM (VIA CARBONIL OXYGEN)

TO CALCIUM (VIA CARBONIL OXYGEN)

CALCIUM (VIA CARBONIL OXYGEN)

TO CALCIUM (VIA CARBONIL OXYGEN)

TO CALCIUM (VIA CARBONIL OXYGEN)

TO CALCIUM (VIA CARBONIL OXYGEN)

TO CALCIUM (VIA CARBONIL OXYGEN)

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TO SELIC SELIC STREET SYSTEM (BY SIMILAR)

TO THER PROSTITE; PROSTITE STREET STREE
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181 DKSYPGRLINIMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGDV-PCDNTTKPGVY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 307:471-479(1995).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- COFACTOR: Binds I calcium ion per subunit (By similarity).
-!- SUBCELDULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.
-!- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                             Galîus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang K., Gan L., Lee I., Hood L.E.; "Isolation and characterization of the chicken trypsinogen gene
                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin II-P29 precursor (EC 3.4.21.4).
                                                                                                                                                                                                                                                            248 AA.
                                                                                                                                                                                                                                                               PRT;
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MEDLINE=95251611; PubMed=7733885;
                                                                                 232 TYICKYVDWIRMIMRNN 248
                                                                                                              240 TKVCHYLEWIRETMKRN
                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                               CHICK
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                                                            IsoId=09H2R5-4; Sequence=VSP_005404;
TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
expressed in the prostate, salivary, and adrenal glands and in the
colon testis and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 IFLLLCVLGLSQAAT -- PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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                                                                                                                                                        SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Gaps
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(BY SIMILARITY).
(BY SIMILARITY).
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B5EBF8D6022786B5 CRC64;
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PRINTS, PR00722; CHYMOTRYPSIN.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SRR; FALSE NEG.

Hydrolase; Serline protease; Glycoprotein; Signal; Zymogen; Alternative splicing.
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GO, GO:0005576; C:extracellular; NAS.
GO, GO:0004252; F:serine-type endopeptidase activity; NAS.
GO, GO:0006508; P:proteolygis and peptidolysis; NAS.
InterPro; IPR00105003; Gys. Ser. trypsin.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001314; Peptidase_SIA.
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             IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
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/FTId=VSP 005405.
V -> G (In isoform 3).
/FTId=VSP 005406.
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BMBL, AF242195; AAG09470.1; -.
EMBL, AF242195; AAG09472.1; -.
EMBL, AF242195; AAG09472.1; -.
EMBL, AF24357; AAG33354.1; -.
EMBL, X75363; CAA53145.1; ALT_SEQ.
HSSP, P00763; 1DPO.
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256 AA;
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111 1
204 2
31 1
52 1
175 2
251 AA;
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                                                                                                                                                                                                                                                                                63 AAHCYKGRIQVRLGEXNIDVQEDSEVVRSSSVIIRHPKY--SSITLNNDIMLIKLASAVE 120
                                                                                                                                                                                                                       120 VTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                                      60 AAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVR 119
                                                                                                                            5 IFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 59
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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
Sequence analysis of chromosome 19q13.4.";
Submitted (CCT-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification and characterization of KLK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."; Genomics 73:117-122(2001).
                                                                                                                                                                                                                                                                    IISNNVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVXIYICKXV
                                                                                                                                                   4 LFLILSCLGAAVAFPGGADDDXIVGGYTCPEHSVPYQVSLNSGYHF-CGGSLINSOWVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLKL6,
                                           196 REQUIRED FOR SPECIFICITY (BY SIMILARITY)
26622 MM; ESEL6B07622B58BE CRC64;
                                                                                                         Gaps
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Catarrhini, Hominidae, Homo.
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                                                                                                         11;
                                                                               41.4%; Score 569.5; DB 1; Length 248; 47.5%; Pred. No. 1e-39; Indels 11 ative 39; Mismatches 78; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yousef G.M., Diamandis B.P.; mapping, and tissue expression "Mollecular characterization, mapping, and tissue expression a hormonally regulated kallikrein-like gene."; Submitted (UUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=21250997; Pubmed=11352573;
Hooper J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A.,
Ashworth L.K., Clements J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like
                                                                                                                                                                                                                                                                                                                                                                                                  251 AA
                             SIMILARITY.
SIMILARITY.
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SIMILARITY
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Mammalia; Butheria; Primates;
NCBI TaxID=9606;
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                                                                                                  Best Local Similarity 47.59
Matches 116; Conservative
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208
187
222
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Homo sapiens (Human).
                             173 1
198 2
196 1
248 AA;
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                                                                                                                                                                                                                                                                                                                                           DWIQ 242
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09P0G3;
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        DISULFID
DISULFID
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                                                                 SEQUENCE
                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 IFLLLCVIGL-----SQAATPKIFNGTECGRNSQPWQVGLFEGTSLR--CGGVLIDHR
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MEDLINE=20545474; PubMed=10969073;
Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K.,
                                                                                                                                                                                                                                                                                   -:- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily
                                                    "Tissue-specific expression patterns and fine mapping of the human "Tissue-specific expression patterns and fine mapping of the human Tailskein (KIK) locus on proximal 19q13.4.";
J. Biol. Chem. 275:379797-37466 (2000).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- TISSUE SPECIFICITY: High expression in brain, bone marrow and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                               fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

GO; GO:0006508; P:proteolyais and peptidolysis; NAS.

InterPro; IPR009003; Cys Ser trypsin.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87; Indels
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Signal, Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KALLIKREIN 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF161221; AAD50773.2; --
EMBL, AF28366; AAK46523.1; --
EMBL, AF293670; AAK46524.1; --
EMBL, AC011473; AAC3260.1; --
EMSP, POOT65; LDPO.
MESOPS, SO1.029; --
Genew, HGNC:6362; KLK14.
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KLK9.

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62 AHCKKPYLWVRLGEHHLMKWEGPEQL----FRVTDFFPHPGFNKDLSAN-DHNDDIMLIR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LGLLCALLSLLAGHGWADT-RAIGAEBCRPNSQPWQAGLFHLTRLFCGATLISDRWLLTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 LRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 WAYPGHISDSMLCAGIWEGGRGSCQGDSGGPLVCNGTLAGVVS-GGAEPCSRPRRPAVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LPRQARLSPAVQPLNLSQTCVSPGMQCLISGWGAVSSPKALFPVTLQCANISILENKLCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVT----HPGY---LGASTSHEHDLRLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein
                                                                                   GO; GO: 0004525; F: Serine-type endopeptidase activity; NAS. GO; GO: 0005508; P: Proteclysis and peptidolysis; NAS. InterPro; PR0010903; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_Si.

InterPro; IPR001254; Peptidase_Si.

InterPro; IPR001254; Peptidase_Si.

Prints, PR00089; trypsin, 1.

PRINTS; PR00020; Trypsin, 1.

RRNART; SM00020; Tryp. SPC; 1.

RROSITE; PS50240; TRYPSIN, DOM; 1.

RROSITE; PS00134; TRYPSIN, DOM; 1.

RROSITE; PS00135; TRYPSIN_BRR; 1.

RROSITE; PS00135; TRYPSIN_SRR; 1.

RROSITE; PS00135; TRYPSIN_SRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27512 MW; F2785245B063E98B CRC64;
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
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tive 32; Mismatches 89;
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                                           MIM; 605504; -. Government; NAS GO; GO:0005576; C:extracellular; NAS
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                       Genew; HGNC:6370; KLK9.
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Matches 119; Conserv
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SEQUENCE FROM N.A.
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KLKD HUMAN
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SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Banganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

Buartes S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;

Sequence analysis of chromosome 19q13.4.";

Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

--- SUBCELLULAR LOCATION: Secreted (Probable).

--- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=20247258; PubMed=10783266; Yousef G.M., Diamandis E.P.; Yousef G.M., Diamandis E.P.; The expanded human kallikrein gene family: locus characterization and molecular cloning of a new member, KLK-L3."; Genomics 65:184-194(2000).
                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cord.
SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in Chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                     250 AA.
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999)
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                                                                                                                                                                                                                                                                                   6-0CT-2001 (Rel. 40, Created)
                                                                            234 ICKYVDWIRMIMRN 247
                                                                                                                     237 LCKYRSWIEETMRD 250
                                                                                                                                                                                                                                        STANDARD;
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15; Gaps

Indels

DB 1; Length 250;

(POTENTIAL)

SIMILARITY) SIMILARITY)

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CHARGE RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-NYPRYILQCAN -> CHEPHARPEAP (IN REF. 3).
                                                                                                                                                             Degeneration of the state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            salivary gland.
-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
       Yousef G.M., Chang A., Diamandis E.P.; ILK-L4, a new kallikrein-like "Identification and characterization of KLK-L4, a new kallikrein-like gene that appears to be down-regulated in breast cancer tissues."; J. Biol. Chem. 275:11891-11898 (2000).
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SIMILARITY).
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-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
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EMBL; AC011473; AAG23259.1; -.

EMBL; AL050220; CAB43320.1; ALT_INIT.

EMBL; AL050220; CAB43320.1; ALT_INIT.

EMBL; P00763; 1DPO.

REROPS; S01.306; -.

REROPS; S01.306; -.

ROHN, 605505; C:extracellular; NAS.

RO; GO:0004252; F:setine-type endopeptidase activity; NAS.

RO; GO:0006508; P:proceolysis and peptidolysis; NAS.

RICHEPPO; IPR001031; Cys Ser trypsin.

RICHEPPO; IPR001254; Peptidase_S1A.

RILLETPO; IPR001314; Peptidase_S1A.
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InterPro; PR00189; trypsin; 1.

PRINTS; PR00722; CHYWOTRYPSIN.

SMART; SW00020; Tryp SPC; 1.

R PROSITE; PS00134; TRYPSIN LDOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R Hydrolase; Serine protease; Glycoprotein; Signal.

TAWNI, 1 16 ROTENTIAL.

ACMNI, R SYSTEM (B
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41.3%; Score 567; DB 1;
Best Local Similarity 46.8%; Pred. No. 1.9e-39;
Matches 116; Conservative 36; Mismatches 80;
MEDLINE=20229789; PubMed=10766816;
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277 AA;
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Gaps

16;

80; Indels

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01-NOV-1997 (Rel. 35, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
117-ypsin I-P38 precursor (EC 3.4.21.4).
Gallus gallus (chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                          180 IISNNVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKXV
                            18 GVSQESS-KVLNTNGTSGFLPGGYTCFPHSQPWQAALLVQGRLLCGGVLVHPKWVLTAAH
                                                             63 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST--SHEHDLRLLRLRLPVRV
                                                                              121 ISSVQPLPLP-NDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR
                                                                                                                                                            137 İGYIĞILPLSHINIRLİPGİTÜRVSGWGITISPOVNYPKILİÇEMILDLRSDEBÜRQVYPĞK
GLSQAATPKIFN------GTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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"Isolation and characterization of the chicken trypsinogen gene
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                                                                                                                                                                                                                                                                                                                                                                           248 AA
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InterPro; IRR00903; Cys_Ser_trypsin.
InterPro; IRR00124; Peptidase_S1.
InterPro; IRR001314; Peptidase_S1A.
Ffan; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0022; Tryp_SPC; 1.
PROSITE; PS00136; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
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MEDLINE=95251611; PubMed=7733885;
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HSSP; P00763; 1DPO.
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01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-1997 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
11779sin I-P1 precursor (EC 3.4.21.4).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
                                                                                                                                                                                                                   REQUIRED FOR SPECIFICITY (BY SIMILARITY). 78B79DD6FE15F0CE CRC64;
                                                                                                                                                                                                                                                                                     Gaps
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- COPACITOR: Binds 1 calcium ion per subunit (By similarity).
-!- COPACITOR: Extracellular.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUB SPECITICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.
-!- SIMILARITY: Belongs to peptidase family S1.
    ACTIVATION PEPTIDE (BY SIMILARITY).
TRYPSIN I-P38.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                           DB 1; Length 248;
                                                                                                                                                                                                                                                                                      86; Indels
                                                                                                                                                                                                                                                           41.2%; Score 566; DB 1;
45.8%; Pred. No. 2e-39;
tive 39; Mismatches E
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MEDLINE=95251611; PubMed=7733885;
                                                                                                                                                                                                                                   26087 MW;
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Matches 116; Conservative
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between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 PVRVTSSVQPLPLPUDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AATLNSYVNTVPLPTSCVTAGTTCLISGWGNTLSSGSLYPDVLQCLNAPVLSSSQCSSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REQUIRED FOR SPECIFICITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                 CHARGE RELAY SYSTEM (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
ACTIVATION PEPTIDE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.1%; Score 565; DB 1; Length 248; 45.5%; Pred. No. 2.4e-39; Live 41; Mismatches 85; Indels
                                                                                                                                                                                                               Pfam; PF00089; trypsin; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00134; TRYPSIN FIS; 1.

Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Calcium-binding; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C4CF589912B23D98 CRC64;
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Last annotation update)
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                                                                                                                      PIR; $55067; $55067.

HSSP; P00765; 1DPO.

MEROPS; $01.151; -.

InterPro; IRR009003; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_51.

InterPro; IRR001314; Peptidase_51A.
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                                                                                                         EMBL; U15155; AAA79912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       llarity 45.5%;
Conservative 4
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236 NYVSWIKTTMSSN 248
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173 1
198 2
196 1
248 AA;
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ID KLKS HUMAN ST

AC Q9Y337; Q9HBGB;

DT 16-OCT-2001 (Rel.)

DT 15-MAR-2004 (Rel.)
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26
65
77
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Matches 115;
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InterPro; IEE.

InterPro; IPR00125-.

InterPro; IPR001314; Pep.

R Pfam; PR00089; trypEsin; J.

R REAM; PR00089; trypEsin; J.

R REAM; PR00089; trypEsin; J.

R RNOITE; PS00135; TRYPEIN HIS; I.

DR RNOITE; PS00135; TRYPEIN HIS; I.

DR PROSITE; PS00135; TRYPEIN HIS; I.

RW Hydrolase; Serine protease; Glycoprotein; Signal.

RW Hydrolase; Serine protease; Glycoprotein; Signal.

RW Hydrolase; Serine protease; Glycoprotein; Signal.

RW Hydrolase; Serine From HIS; I.

RALLIKREIN S.

CHARGE RELAY SYSTEM (BY F.

CHARGE RELAY SYSTEM (BY F.

SIMILARITY.
                                                                                 MIN, 00.00035, ...
GO; GO:0005515, C:extracellular space; TAS.
GO; GO:000522; F:serine-type endopeptidase activity; NAS.
GO; GO:000554; P:spidermal differentiation; TAS.
GO; GO:0005508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR00134; Peptidase_S1.
   MEKUPS; S01.017; -.
Genew; HGNC:6366; KLK5.
                                                                   MIM; 605643;
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KLKA_HUMAN
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=23388257; PubMed=12477932;

MEDLINE=23388257; PubMed=12477932;

MEDLINE=23388257; PubMed=12477932;

MEDLINE=2338257; PubMed=12477932;

MEDLINE=2338257; PubMed=12477932;

MEDLINE=2338257; PubMed=12477932;

MEDLINE=2338257; PubMed=12477932;

MEDLINE=2338257; PubMed=12477932;

MEDLINE=2338257; PubMed=124, Mance T.M. Scheetz T.E., Scheetz T.E., Scheetz T.E., Scheetz T.E., Scheetz T.E., Scheetz T.E., Manch D.E., McKernan K.J., Malek J.A., Gabarathe P.H., Rabarathe P.H., Madan A., Malek J.A., Gabarathe P.H., Glibbs R.A., Willalon D.K., Murray D.M., Scheern E.D., Dickson M.C., Sanchez A., Muthing M.M., Green B.D., Dickson M.C., Bulterfield Y.S.N., Krzywinski M.I., Skalakka U., Smailus D.E., Brock Manch M. Schein J. Medel M. Marra M.A., Schein J. Medel M. Marra M.A., Schein J. Medlida analysis of more than 15,000 full-length human and mouse cDNA sequences.", Medligual M.A., Schein J. A., Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Schein J. Sc
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Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme) (Kallikrein-like protein 2) (KLK-L2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
                                                                                                                                                                                                                                                                         ASQUENCE FROM N.A.

TISSUE-Stratum corneum;

MEDLINE-9944553; PubMed=10514489;

Brattsand M., Egelrud T.;

"Purification, molecular cloning, and expression of a human stratum corneum trypsin-like serine protease with possible function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDIANS=20118165, PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE=20510030; PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Gan E., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene "Luster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      desquamation.";
J. Biol. Chem. 274:30033-30040(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999)
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EMBL; AF135028; AAD25429.1; -.
EMBL; AF243527; AAG33358.1; -.
EMBL; BC008036; AAH08036.1; -.
                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                          Homo sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                 KLKS OR SCIE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 HYSLSPVYESGQQMEQGVKSIPHPGY.-SHPGHSNDLMLIKLNRRIRPTKDVRPINVSSH 177
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kallikrein 10 precursor (EC 3.4.21.-) (Protease serine-like 1) (Normal epithelial cell-specific 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 SQAATPKIFNGTECGRNSQPWQVG-LFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 EHSLSQLDWTEQIRHSGF-SVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 CPSAGTKĆLVSGWGTTKSPQVHPPKVLQCLNISVLSOKRCEDAYPRQIDDTMPCAGDKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 QDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                    SIMILARITY).
SIMILARITY).
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BY SIMILARITY.
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293
1108
1153
2245
2206
1231
266
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208
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25
293 AA;
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23
108
1153
245
73
93
1185
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P00763; 1DPO.

EMBL; HSSP;

H., McCuaig J.,

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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschuls T.E., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschuls R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
HOpkins R.F., Jordan H., Moore T., Mans S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Norlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevochenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Roberstion and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liamerdin J.E., McCready P.M., Skowronski E., Viewanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
Duarte S., Iucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      progression.
SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
MEDLINE-96320486; PubMed-8764136;
Liu X.-L., Wazer D.E., Watanabe K., Band V.;
"Identification of a novel serine protease-like gene, the expression
of which is down-regulated during breast cancer progression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goyal J., Smith K.M., Cowan J.M., Wazer D.E., Lee S.W., Band V.; "The role for NES1 serine protease as a novel tumor suppressor."; Cancer Res. 58:4782-4786(1998).
                                                                                                                                                                                                                "Structural characterization and mapping of the normal epithelial cell-specific 1 gene.";
Biochem. Biophys. Res. Commun. 247:580-586(1998),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Has a tumor-suppressor role for NES1 in breast and
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                                                                                                                                SEQUENCE FROM N.A.
MEDINE=9931170; PubMed=9647736;
Luo L.-Y., Herbrick J.A., Scherer S.W., Beatty B., Squire J.,
Diamandis E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20510030; PubMed=11054574;
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                                                                                       Cancer Res. 56:3371-3379(1996)
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001254; Peptidase_Si.
InterPro; IPR001254; Peptidase_Si.
InterPro; IPR001254; Peptidase_SiA.
InterPro; IPR001314; Peptidase_SiA.
InterPro; IPR001314; Peptidase_SiA.
INTERPOSED PR001314; PRYPSIN.
INTERPOSED PR00132; CHYMOTRYPSIN.
INTERPOSED PR00134; TRYPSIN DOM; I.
IPROSITE; PS00134; TRYPSIN HIS; I.
IPROSITE; PS00134; TRYPSIN HIS; I.
IPROSITE; PS00135; TRYPSIN ER; FALSE NEG.
Hydrolase; Serine protease; Glycoprotein; Signal; Anti-oncogene.
SIGNAL.
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P -> L (IN REF. 3 AND 4).
82A2507379BAB313 CRC64;
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GO; GO:0008236; F:serine-type peptidase activity; TAS
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EMBL; AF055481; AAC14266.1; --
EMBL; AF054357; AAG33363.1; --
EMBL; AC011473; AAG32256.1; --
EMBL; BC002710; AAH02710.1; --
HSSP; PO0763; IDPO.
MEROPS; S01.246; --
Genew; HGNC:6358; KLKIO.
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P70059; 01-NOV-1997 (Rel. 35, Created)

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                                                                                                                                                                                                                                                                                                                                          Wang K., Lytle L., Gan L., Hood L.E.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBV databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: Belongs to peptidase family S1.
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin precursor (EC 314.21.4)
Xenopus laevis (African clawed frog).
Xenopus laevis (African Clawed frog).
Ambribia; Metazod; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Barrachia; Amura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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Best Local Similarity 45.0%; Pred. No. 3.5e-39;
Matches 112; Conservative 46; Mismatches 83;
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Search completed: June 16, 2004, 20:33:11 Job time : 18 secs

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GenCore version 5.1.6
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This clone (DKF2068H1078) is available at the RZPD in Berlin. Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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//organism="Homo sapiens"
//dnol_type="mkNA"
//db_xref="texon:9606"
/clone="DKFZp686H1078"
/clone="DKFZp686H1078"
/clone_lib="buman endometrium carcinoma cell line"
/clone_lib="666 (synonym: hlcc3). Vector pSportl_Sfi; host DH108; sites SfilA + SfilB"
//dev_stage="adult"
/ 102
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HOmo sapiens mRNA; cDNA DKFZp686H1078 (from clone DKFZp686H1078).
BX648580
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Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
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The German Human CDNA Consortium Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OS Homo sapiens (human)
PN 025262600-A/3
PD 29-JAN-2002
PF 04-FEB-1999 JP 2000530597
PR 06-FEB-1999 US 60/073961
PI STEVEN M RUBEN,JIAN NI
PC
C12N9/64,A61X38/48,A61P7/02,A61P7/04,A61P7/06,A61P29/00,A61P31/PC
                                                                                                                                    PAT 18-SEP-2002
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1 (bases 1 to 840)

Ruben,S.M. and Ni,J.

Ruben,S.M. and Ni,J.

Patent: JP 20050cease and serpin polypeptide
Patent: JP 20050c200-80, 3 29-JAN-2002;

HUMAN GENOME SCIENCES INC
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C12N1/21,
PC C12N5/10,C12N15/09,C12Q1/37,A61K37/547,C12N5/00,C12N15/00
Human serine protease and serpin polypeptide
FW Key Location/Qualifiers
FT CDS (115)..(603).
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Indels
                                                                                                                                    linear
                              Human serine protease and serbin polypeptide.
BD130047
BD130047.1 GI:23224992
JP 2002502600-A/3.
Homo sapiens (human)
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46.4%; Score 506.4; DB 6;
Best Local Similarity 97.9%; Pred. No. 1.1e-104;
Matches 513; Conservative 0; Mismatches 11;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AUTHORS
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                                                                                             RESULT 5
BD130047
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                                                                                                                                                        CCTGCCAGCCCTTCTAAGACCCACGAGGGGGGGGAGAGAGTGTGCAATAGTCTGGAATA 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCAT 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGA 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603
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                                                                                                 586 CCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACT 645
                                                                                                                                                                               CCTGCCAGCCCTTCTAAGACCCACGAGGGGGGGGAGAAGTGTGCAATAGTCTGGAATA 705
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                    526 CCACCTCCACCCCCACCCCTAACTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCT
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                                                                             CCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACT
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46.4%; Score 506.4; DB 6; Length 840;
Best Local Similarity 97.9%; Pred. No. 1.1e-104;
Matches 513; Conservative 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 840)

Ni,U. and Ruben,S.M.

Win. serine protease and serpin polypeptides

Patent: US 6566498-A 5.20-MAY-2003;
                                                                                                                                                                                                                                    1058 AATATAAATGAAGGAGGGCAAAAAAAAAAAAA 1091
                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                    AR337568 840 bp
AR327568 8566498
AR337568.1 GI:33723963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
/wol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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AR337568
LOCUS
DEFINITION
ACCESSION
VERSION
KRYWORDS
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PRI 26-JUN-2000
                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 9120)
Yousef, G.M., Scorilas, A. and Diamandis, B.P.
                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 9120)
Yousef,G.M., Scorilas,A. and Diamandis,E.P.
Direct Submission
Submitted (01-JUL-1999) Pathology and Laboratory Medicine, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario MSG 1x5,
                                                                                                                                                                                                                                                         Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human kallikrein gene family Genomics 63 (1), 88-96 (2000)
                                                                                                     protease (TLSP) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          762 GTCCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGGAAGTATGIGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="trypsin-like serine protease"
join (4224. 4263,5061. .5217,5545. .5810,6627. .6763,
1958. .7310)
jene="TLSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGAGTCCTTCAAGGTCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 GICCTGGGGGTCIGIGGGGCCCTGTGGAAGATGGCATCCCTGGAGTCACACCTATAT
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6627. .6763,7158. .7622)
/gene="TLSP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="kallikrein-like serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 373.2; DB 9;
Pred. No. 2e-74;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .9120
/organism="Homo sapiens"
                                                                                        AF164623 9120 bp
Homo sapiens trypsin-like serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="19q13.3-q13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                    617
                                                                                                                                              AF164623.1 GI:5713130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2313. .7622
/gene="TLSP"
                                                                                                                                                                         Homo sapiens (human)
    602 ATGGTGTGTATCCGGG
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Best Local Similarity 99.2
Matches 375; Conservative
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                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGACTTTGGAAGTGACCCACCATGGGGCTCAGCATCTTTTTGCTCCTGTGTTCTTG 126
TGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCACGAGCACGACCTCCGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             724 AACITITAACTCCCGCCCGCCCTCTAAGACCCACGAGGGGGGGGGAGAGTGTGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTCAGCCAGGCACACCCACACCGAAGATTTTCAATGGCACTGAGTGTGGGGCGTAACTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCGTGGCAGGTGGGGCTGTTTGAGGCCACCAGCCTGCGCTGCGGGGGTGTCCTTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACAGGTGGGTCCTCACAGCGGCTCACTGCAGCGGCAGCAGGTACTGGGTGCGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 619;
                                                                                                  1048 GTCTGGAATAAAATGAAGGAGGGCCAAAAAAAAAAAA 1091
                                                                                                                              Indels
                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 493.2; DB 6;
Pred. No. 1.1e-101;
0; Mismatches 8;
                                                                                                                                                                                                   DNA
                                                                                                                                                                                                   9 bp DN
6331427.
                                                                                                                                                                                                                                                                                                                                         Protease homologs
Patent: US 6331427-A 139 18-DEC-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
/wol_type="genomic DNA"
                                                                                                                                                                                                  619
US 6
                                                                                                                                                                                                AR263961
Sequence 139 from patent
AR263961
                                                                                                                                                                                                                                         AR263961.1 GI:28075965
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.2%;
Best Local Similarity 97.7%;
Matches 543; Conservative 0
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Robison, K.E.
                                                                                                                                                                                                                                                                                                                                                                                     1. .619
                                                                                                                                                                                                                                                                                                 Unclassified.
                                                                                                                                                                                                                                                                     Unknown.
                                                                                                                                                                                                                                                                                     Unknown
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="WGLSIFILLCVLGLSQAATPKIFNGTECGRNSQEWQVGLFEGTS
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                                                       join (3743. 3840, 3995. 4055, 4496. 4655, 6500. 6759, 7714. 7847, 9178. 9293, 9423. 9543)
// product="Kallikrein-like protein 5-related protein 1" join (3743. 3840, 3995. 4050, 4496. 4655, 7714. 7847, 9178. 9543)
// product="Kallikrein-like protein 5-related protein 2" join (4014. 4050, 4496. 4655, 6500. 6759, 7714. 7847, 9178. 9293, 9423. 9480)
// note="Kik is-related protein 1; kallikrein-like serine protease; alternatively spliced"
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protease; alternatively spliced"
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9178. .9333)
/note="KLK-L5"
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7714. .7847,9178. .9543)
/product="kallikrein-like protein 5"
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/db_xref="GI:6166249"
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                 CTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGGCCCTCAGAGCACCAATATCTCCTC 941
                                        Anticancer Res. 79, 2843-2852 (1999)
C bases 1 to 11820)
Diamandis E.P., Yousef, G.M., Luo, L.Y., Magklara, A. and Obiezu, C.V.
The new human kallikrein gene family: implications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 2909 to 7847)
Yousef,G.M., Luo,L. and Diamandis,E.F.
Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yousef,G.M., Magklara,A., Scorilas,A. and Diamandis,E.P. Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-MAR-1999) Pathology and Laboratory Medicine, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
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Yousef,G.M., Magklara,A. and Diamandis,E.P.

Direct Submission

Submitted (01-NOV-1999) Pathology and Laboratory Medicine, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario MSG 1X5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 11820) Yousef. G.M., Magklara, A. and Diamandis, E.P. KLk-L5 is a novel serine protease and a new member of the human kallikrein gene family-differential expression in breast cancer
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Homo sapiens kallikrein-like protein 5 gene, alternative splice
products, complete cds.
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On Nov 1, 1999 this sequence version replaced gi:4589276.
Location/Qualifiers
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Yousef,G.M., Magklara,A. and Diamandis,E.P.
Direct Submission
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PWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPBQE1PVVQ
SIPHPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTV
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TLQCANISILENKCHWAYPCHISDSWLCAGIWBGGRGSCQGDSGGPLVCNGTLAGVV
SGGAPCSRFRRPAVYTSVCHYLDWIQEIMEN"
                                                                                                                                                                                                                                                                                                                                                                               note="kallikrein 9; synonyms: KLK-L3, kallikrein-like
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(2594. .3341,3785. .3921,6539. .6804,
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9264. .9420,9586. .9628))
/gene="KLK9"
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                                                                                                                                                                                                                                                          family="MSR1" cment ()
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'product="kallikrein 9"
                                                                                                                     /rpt_family="MSR1"
complement(1374. .1554)
/rpt_family="MSR1"
1723. .1754
                                                                                                                                                                                                                                                                                                                  complement (2594. .9715)
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5370_ .540^
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/rpt_family="MER104"
6422. .6520
/rpt_family="GA-rich"
7221. .726
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rpt_family="GA-rich"
1140. .4449
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529. .4812
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/rpt_family="AluJo"
5605. .571?
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/rpt_family="CT-rich"
5346. .6411
                                                                                                                                                                                                                                  /rpt_family="(TCC)n"
complement(1791, .22:
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5044. .6235
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8634_ .8919
/rpt_family="MER33"
10629_ .10758
/rpt_family="L2"
10755_ .10905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="AluSx"
450. .4483
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complement(5043. .5;
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7840. .7938
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/rpt_family="MSR1"
3558. .3700
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rpt_family="MSR1"
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878. .6014
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3130. .8448
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PRSS19, HNP; protease, serine, 19 (neuropsin/ovasin)"
complement(join(<77. 339,505. 664,1179. 1256,1613. 1783))
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Submitted (12-OCT-2000) DOE Joint Genome Institute, Lawrence
Submitted (12-OCT-2000) DOE Joint Genome Institute, Lawrence
Livermore National Laboratory, Livermore, CA 94550
Divoct 12, 2000 this sequence version replaced gi:7458725.
Map and sequence oriented from centromere to q-telomere. BC349142
(CTC-518B2) overlaps BAC BC68745 (CTP-147C22, ACO11483) on the left
from bases 1 to 2,226 of this accession, and overlaps BAC BC692989
(CTD-3187F8, AC063977) on the right from bases 120,922 to 132,323
of this accession. Additional chromosome 19 map and sequence
PRI 12-OCT-2000
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Homo sapiens chromosome 19, BAC BC349142 (CTC-518B2), complete
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/gene="KLK8"</pre>
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clone_lib="CIT-HSPC"
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http://www-bio.llnl.gov/bbrp/genome/genome.html.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="1943.4"
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DOB Joint Genome Institute.
Direct Submission
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KEYWORDS
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COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

F. (Dases 1 to 230000)

Gan,L., Lee,I., Smith,R., Argonza-Barrett,R., Lei,H., McCuaig,J., Moss,P., Paeper,B. and Wang,K.
Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region

Gene 257 (1), 119-130 (2000)

D. 11054574

E. 20510030

E. 20510030

B. 20510030

Can,L., Lee,I., Smith,R., Argonza-Barrett,R., Lei,H., McCuaig,J., Moss,P., Paeper,B. and Wang,K.

Direct Submission

L. Submitted (1994RR-2000) Chiroscience R & D Inc., 1631 220th St. SE, Medical Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
       29488 GTCCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATAI 29429
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Homo sapiens serine protease gene cluster, complete sequence.
AF243527
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                                                                                                                                                                                                                                                                                                                            19308 CATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTG
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                                                                                                                                                                                                                                                                                       942 CATCACTICCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTG
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9482, 9641,11472, >11517)}
/gene="KLK1"
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/protein_id="AAG33353.1"
/db_xref="GI:11244758"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13"
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Location/Qualifiers
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KEYWORDS
SOURCE
ORGANISM
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|Protein_id="AAG23256.1"
| Drotein_id="CT:1079395"
| Aranslation="MRAPHIHISAASGARALAKILPII.MAQIWAAEAAII.PQNDTRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEAYGSPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAÄHCGNKPLWARVGDDHLL
LLQGEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVLGPRVRALQLPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCAQPGDQCQVAGWGTTAARRVKYNKGLTCSS1T1LSPKECEVFYPGVYTNMM1CAGL
DRGQDPCQSDSGGPLVCDETLQG1LSWGVYPCGSAQHPAVYTQ1CKYMSWINKVIRSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="kallikrein 10; synonyms: NES1, PRSSL1"
complement(join(14351. .15033,15498. .15631,15963. .16237,
17191. .17371,19124. .19220,19708. .19779))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .15631,15963. .16237,
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/standard_name="stSG30247"

/note="RH48452, WIRF-3662-STS"

complement (14432. 14604)

/rpt_family="MIR"

complement (join(14881. 15033,15498. 117191)

/gene="KLKIO"
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codon start=1
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/ rpt family="L2"
complement (12694. 12976)
/ rpt family="L2"
/ rpt family="L2"
                                                                                                      /rpt_family="(TTTG)n"
complement(11133. 11411)
/rpt_family="AluSg"
11412. 11515
/rpt_family="MIR"
                                                                                                                                                                                                                                                          /rpt_family="AluSx"
complement(11989. .12069)
/rpt_family="MIR"
complement(12070. .12390)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="Alusq"
ement()42=7
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ement / 1.
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17797. .1791
                                                                                                                                                                                                                                                                                                                                                                                   complement (12391, .12498)
/rpt_family="MIR"
12503. .12606
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complement(14351. .19779)
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15715. .15967
/rpt_family="MSR1"
complement(16473. .16810
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/product="KLK10 mRNA"
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/rpt_family="AluJo"
17913. .17932
/rpt_family="(CAA)n"
/rpt_famlx,
10976..11096
/rpt_famlly="MIR"
-^^7..11128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13287. 13393 / rpt family="L2" complement (13507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="L2"
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Best Local Similarity 99.2
Matches 375; Conservative
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SE,

/translation="MWFLVLCLALSLGGTGAAPPIOSRIVGGWECEOHSOPWOAALYH FSTFQCGGILVHRQWVLTAAHCISDNYQLWLGRHNLFDDENTAQFVHVSESFPHPGFN MSLLENHTRQADEDYSHDLMLLRLTEPADTITDAVKVVELPTEEPEVGSTCLASGWGS

762 GTCCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATAT 821

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/translation="MKKLMVVISLIAAAWAEEQNKLVHGGPCDKTSHPYQAALYTSGH
LCGGVLIHPLWVLTRAHCKKPULQVFLGKHNLRQRESSQEGSSVRAVIHDDYDAAS
HDQDIMLLRLARPAKLSELIQPLPIBRDCSANTTSCHILGWGKTADGDFPDTIQCAYI
HLVSREBCHAXPGQTTQNMLCAGDBKYGKDSCQGDSGGFLVCGDHLRGLVSWGNIPC
GSKERPGVYTNVCRYTNWIQKTIQAK"
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/bb_xxef="G1:11244766"
/db_xxef="G1:11244766"
/db_xxef="G1:112477676"
/db_xxef="G1:11247676"
/db_xxef="G1:112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mwvlcAlitalligvtdarsddsssriingsdcdwhtqpwqaal
LLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPVYESGQQNFQGYKSIPH
PGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPSAGTKCLVSGWGTTKSPQVHF
PKYLQCLNISVLSQKRCEDAYPRQIDDTWFCAGDKAGRDSCGGDSGGPVVCNGSLQGL
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VALLSGNQLHCGGVLVNERWYLTAAHCKNURETYYHLGSDTLGDRAGARTKASKEFRHW
SYSTQTHVNDLMLVKLNSQALLSSNYKKRLEPSCREPGTTGTVSGNGTTTSPDVTFP
SDLMCVDVKLISPQCTRVYKDLLESNMLGAGIPDSKKNACNGDSGGPLVCRGTLGGL
VSWGTFPCGQPNDFGYYTQVCKFTKNINDTMKKHR"
VSWGTFPCGQPNDFGYYTQVCKFTKNINDTMKKHR"
187865. .188127,188293. .1884088,185635. .185768,
/product="neulogsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MARSLLIPLQILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQ
                                                                                                                                protease"
                                                                                                                                                                                                                                                                                                                                                                 'product="stratum corneum trypsin-like serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(146834. .146986,149628. .149764,
151186. .151433,155052. .155208,155948. .155987))
/note="serine protease; also called neurosin or zyme"
/codon_start=1
/product="protease M"
/product="approtease M"
/protein_id="AAG33359.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(<146834. 146986,149628. .149764,
151186. .151433,155052. .155208,155948. .>155987))
/product="procease M"
                              .>140303))
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                                                                                                 complement (join(131301. .131456,135310. .136443, 136529. .136785,137525. .137690,140255. .140303))
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187865. .188127,188293. .188452,188967. .189036))
/note="serine protease; also called ovasin"
/codon_start="
/product="neuropsin"
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complement(join(165420. 165575,167672. 167808,
168124. 168371,169651. 169798,170211. 170283))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(190980. .191129,191573. .191709, 194324. .194589,197048. .197204,197370. .197412))
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/product="stratum corneum chymotryptic enzyme"
/protein_id="AAG33360.1"
/db_xref="GI:11244765"
                    .136785,137525. .137690,140255.
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                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAG33358.1"
/db_xref="G1:11244763"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="KLK7"
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17614. .>47769)
'gene="KLK3"
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CNGVLQGITSWGPEFCALPEKPAVYTKVVHYRKWIKDTIAANP
EPENFSFPDDLQCVDLKILPNDECKKAHVQKVTDFMLCVGHLEGGKDTCVGDSGGPL
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GLVSFGKAPCGQVGVPGVYTNLCKFTEWIEKTVQAS"
complement (<131301. ,>140303)
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VRHPEYNRPLLANDLMLIKLDESVSESDTIRSISIASASQCPTAGNSCLVSGWGELANGR
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96919. .97081,98345. .>98405))
/product="serine protease"
complement (join (94602. .94754,96027. .96163,96247. .96497,96319. .97081,98345. .98405))
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prostate specific antigen"
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<42595. ,>47769
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SGGAEPCSRPRRPAVTSVTCHYLDWIORIMBN"
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Pan troglodytes clone RP43-63K10, WORKING DRAFT SEQUENCE, 10
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                34.2%; Score 373.2; DB 9; Length 230000; 99.2%; Pred. No. 1.7e-74; ive 0; Mismatches 3; Indels 0;
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HTG; HTGS PHASE2; HTGS_DRAFT.
Pan troglodytes (chimpanzee)
Pan troglodytes
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2 (bases 1 to 174724)
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Matches 375;
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**NOTE: This is a 'working draft, sequence. It currently consists of 10 contigs. Gaps between the contigs. **are represented as runs of N. The order of the piaces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be preserved.

**Paralle sequence as soon as it is available and the accession number will be preserved.

**A7271 47270 contig of 47270 bp in length 47271 47370: gap of unknown length 147271 47370: gap of unknown length 147271 47370: gap of unknown length 15815 contig of 1745 bp in length 15815 contig of 4196 bp in length 15846 61150: gap of unknown length 15846 61150: gap of unknown length 15847 55446: gap of unknown length 15834 65345 contig of 6109 bp in length 15837 65446: gap of unknown length 15834 68233: gap of unknown length 15834 68233: gap of unknown length 15834 68233: gap of unknown length 15834 68233: gap of unknown length 15834 68233: gap of unknown length 15834 68233: gap of unknown length 15834 68233: gap of unknown length 15838 174724: contig of 1894 bp in length 159208 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 129209 174724: contig of 4510 bp in length 174724: contig of 4510 bp in l
Direct Submission
Submitted (14-JUN-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 14, 2003 this sequence version replaced gi:29725783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 172841 bases at least Q40
Consensus quality: 173490 bases at least Q30
Consensus quality: 173737 bases at least Q20
Insert size: 150000; agarose-fp
Insert size: 173824; sum-of-contigs
Quality coverage: 13.73x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                     Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: dxz
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1. .79098
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Pan troglodytes
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8524. .88837
/note="assembly_fragment"
88938. .129108
/note="assembly_fragment"
/note="assembly_fragment"
/note="clone overlaps with Genbank Accession Number
/note="clone CH251-126024 (center project name dxa)"
              AC130782 clone CH251-355A20 (center project name dhz)"
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note="clone overlaps with GenBank Accession Number
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                                                                                                                                      58216. .61050 '-
/note="assembly_fragment"
61151. .65346
                                                                                                                                                                                                                           note="assembly_fragment"
1637. .83139
note="assembly_fragment"
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/note="assembly_fragment"
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65447. .71536
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                                              'note="assembly_fragment
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                                                                     clone_end:T7
vector_side:left"
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Best Local Similarity 98.4%;
Matches 372; Conservative
                                 . .47270
                                   misc_feature
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AC130782.2 GI:25167101 HTG; HTGS_PHASE2; HTGS_DRAFT. Pan troglodytes (chimpanzee)

DEFINITION
ACCESSION
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KEYWORDS
SOURCE

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Rukaryota, Wietazoa; Chordata, Carminata; Wertebrata; Pantel-centum; Manmalia; Butheria; Printer, Mantel, Butheria; Printer, Mantel, Butheria; Printer, Mantel, Butheria; Printer, Mantel, Butheria; Printer, Mantel, Butheria; Printer, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mantel, Mante
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148483 CTCCACCCCACCCCTTAGCTTGGGTACCACTCTGGCCCCCAGAGCACCAATATCTCCTC 148424
                                                                                                                       148423 CATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTG 148364
                                                                                                                                                                                                                                                                                         142334 bp DNA linear HTG 17-AUG-2000 Homo sapiens chromosome 19 clone RP11-10111, WORKING DRAFT SEQUENCE, 32 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Materston, R.H.

Direct Submission
Submission
Submission
Submission
Moiversity School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9653152.
                                                        CATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will be preserved.
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Unpublished
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AC073185.4 GI:9838034
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                             148303 TAATGAAGGAGGGCCA 148286
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Waterston, R.H.
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1553
2738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 200792;
   contig of 35566 bp in length
gap of unknown length
contig of 9945 bp in length
contig of 5150 bp in length
contig of 5150 bp in length
gap of unknown length
contig of 36694 bp in length
contig of 36694 bp in length
contig of 3468 bp in length
contig of 34168 bp in length
gap of unknown length
contig of 14719 bp in length
contig of 14719 bp in length
contig of 14719 bp in length
contig of 14719 bp in length
contig of 14584 bp in length
contig of 1682 bp in length
contig of 682 bp in length
contig of 682 bp in length
contig of 682 bp in length
contig of 682 bp in length
contig of 1839 bp in length
contig of 1839 bp in length
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Pred. No. 2.2e-73;
                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
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/clone="CH251-355A20"
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83668. .88817
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15980. .174698
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174799. .186382
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                                                                                                                                                                                                                                                                                                                                                                                                           contig of 1306 by in length contig of 2961 by in length contig of 2961 by in length gap of unknown length in length of 2961 by in length contig of 2988 by in length contig of 2888 by in length gap of unknown length length contig of 3209 by in length gap of unknown length length contig of 3962 by in length gap of unknown length gap of unknown length contig of 3962 by in length gap of unknown length contig of 3965 by in length gap of unknown length contig of 3965 by in length gap of unknown length gap of unknown length contig of 4636 by in length gap of unknown length gap of unknown length contig of 4439 by in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length
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132749: gap of unknown length
142334: contig of 9585 bp in length.
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4766. .6054
/note="assembly_name:Contig29"
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note="assembly_name:Contig26"
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/note="assembly_name:Contig27"
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of 1769 b
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of 2135 b
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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10930 GTCCTGGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATAT 10871
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                                                                                                                                    /5171. .18476 --
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/note="assembly_name:Contig33"

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/note="assembly_name:Contig48"
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22124. .132649
note="assembly_name:Contig57"
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132750. .142334
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note="assembly_name:Contig47"
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15194, .122023
              note="assembly_name:Contig30"
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                                                                                                                        CATCACTTCCCCTAGCTCCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTG 1001
                                                                                                                                                                                            1002 CCAGCCCTTCTAAGACCCCACGAGCGGGGTGAGAAGTGTGCAATAGTCTGGAATAATA 1061
                                                                                                                                                                                                                                                                                                                                                                                        linear PAT 25-JAN-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams, L. T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B. Human genes and gene expression products
Patent: WO 0102568-A 1410 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | GGGTGACCTCTGAGATTCCCC-TTTTCCCCCAGACTTTGGAAGTGACCCACCATGGGGCT
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                                                      CTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCCTCAGAGCACCAATATCTCCTC
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                                                                                                                                                                                                                                                                       1062 TAAATGAAGGAGGGCAA 1079
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Matches 308; Conservative
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Cercopithecinae; Papio.

Cercopithecinae; Papio.

S Akhter.N., Antonellis, Papio.

S Akhter.N., Buncaelly, R.W., Byele, K., Beckstrom-Sternberg, S.W., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Hangol, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Lario, P., Han, J., Hansen, N., Maduro, O.L., Maduro, V.B., Marqulies, E.H., Masiello, C., Maskeri, B., McDowall, J., Parason, R., Portnoy, M. E., Prasada, B., McDowall, J., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.

In Unpublished
AC130188 176647 bp DNA linear HTG 14-NOV-2002
Papio amubis clone RP41-421P3, WORKING DRAFT SEQUENCE, 12 ordered
                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contrig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misssemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-AUG-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 176647)
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Submitted (14-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Nov 14, 2002 this sequence version replaced gi:22138439.
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Insert size: 175547; sum-of-contigs
Quality coverage: 8.76x in Q20 bases; agarose-fp
Quality coverage: 9.39x in Q20 bases; sum-of-contigs
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Contact: nisc_zoo@nhgri.nih.gov
Center project Information
Center project name: dsr
Center clone name: 421P03
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                                                                                                                                                                   AC130188.2 GI:24960890
HTG; HTGS PHASE2; HTGS DRAF
Papio anubis (olive baboon)
Papio anubis
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Indels

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116911. .176647
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125307. .127021
* consists of 12 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 6527 6626; gap of unknown length
* 6627 18812; contig of 6526 bp in length
* 6627 18812; contig of 12186 bp in length
* 61781 61780; contig of 12186 bp in length
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Location/Qualifiers
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170283. 176647
'note="assembly_fragment
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Score 294; DB 2; Length 176647; Pred. No. 1.9e-56;

26.9%; 91.3%;

Query Match Best Local Similarity

vector side:right"

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                                   TGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGAGTCCTTCAAGGTCTGGT
Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aaa77671 Human PRO Aaa37075 Human PRO Aa437075 Human PRO Aaf54341 DNA encod Acd68378 Novel hum Ach04480 Human CDN Human Human Human Human Human Human Human Human Human Human Human Human Human Novel Human Description Acho4480 I Acd68024 I Add70802 I Add39785 I Add39318 I Add39308 I Add39318 I Add304082 I Add504082 I Ade20095 I Ade20095 I Ade20095 I Ade20095 I Ade20095 I Ade20096 I Ade20096 I Ade20096 I Ade39914 I Aal59914 I Aax8906 I SUMMARIES ADD40262 ADE50483 ADE20095 ADE50006 ACH04480 ACD68024 ADC18062 ADD70708 ADD39785 ADD70231 ADD38352 ADD39308 ADD38831 AAL59914 ABK94900 AAX80906 AAF54341 ACD68378 AAH98653 4AA37075 AAA77671 AAC58114 Query Match Length DB 1091 1091 1091 1091 1091 1091 1091 1091 1091 1091 1091 1091 1091 1091 109 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 68.4 66.6 46.4 00 100. 10091 10091 10091 10091 10091 10091 10091 10091 10091 10091 968 746.6 727 506.4 Score Result No.

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ALIGNMENTS

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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
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Kuo SS, Paoni NF;
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Klein RD,
                                                                         Human PRO1303 cDNA sequence SEQ ID NO:202.
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Gurney AL,
                  BP
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99US-0123957P.
99US-0131445P.
99US-0134287P.
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99WO-US020594.
99WO-US020944.
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99WO-US023089.
99US-0162506P.
                 AAA77671 standard; cDNA; 1091
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Goddard A, Godowski PJ,
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08-SEP-1999;
13-SEP-1999;
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28-APR-1999;
14-MAY-1999;
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08-MAR-1999
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26-JUL-1999;
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                                                                                                                                                                                                                          The present invention describes mucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy. For polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24188 to AAB24435 represent mucleotide and protein sequences used in the exemplification of the
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Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Indels 0;
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Wood WI;
Williams PM,
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                                           WPI; 2000-412154/35.
P-PSDB; AAB24428.
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                                           The present invention describes an antibody that binds to a human protein (I) selected from: PRO381, PRO1269; PRO1101, PRO1755, PRO1780; PRO3434; PRO1927; PRO1567, PRO1956; PRO1293; PRO1936; PRO4344; PRO4934; PRO4927; PRO1956; PRO1096; PRO1036; PRO49497; PRO4957; PRO1565; PRO1096; PRO2038; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Complex formation when the antibody is contacted with test cells. Complex formation when the antibody is contacted which hybridises to genes the antibodies, or an antisense oligomucleotide which hybridises to genes encoding (I). Can be used to inhibit tumour growth, preferably by inducing (I). Can be used to inhibit the present invention can be used to inducing cell death. Methods from the present invention and be used to inducing cell death. Methods from the present invention probes used in to AAC5812 and AAB24021 to AAB24040 represent human PRO polymocleotide and AACS812 and AAB24021 to AAB24040 represent human PRO polymocleotide and protein sequences given in the exemplification of the present invention
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Best Local Similarity 100.0%; Score 1091; DB 3; Length 1091;
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Indels 0;
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98US-0105697P.
98US-0105807P.
98US-0106881P.
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receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA31145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.
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02-DEC-1999; 99W0-USO28651.

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Williams PM, Wood WI;
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Fong S; Hillan KJ; Watanabe C

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The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used used either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nuclacids may also be used in gene therapy
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24-FEB-2000; 2000WO-US004342.

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02-MAR-2000; 2000WO-US005681.

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17-MAY-2000; 2000WO-US013705.

22-MAY-2000; 2000WO-US014941.

30-MAY-2000; 2000WO-US014941.

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23-AUG-2000; 2000WO-US01352.

24-AUG-2000; 2000WO-US02352.

10-NOV-2000; 2000WO-US02352.

10-NOV-2000; 2000WO-US036652.

10-MAR-2001; 2001WO-US015666.

01-UTN-2001; 2001WO-US01666.

20-UTN-2001; 2001WO-US011669.

20-UTN-2001; 2001WO-US01166.

09-UTL-2001; 2001WO-US01166. (GETH) GENENTECH INC. WPI; 2003-585293/55. P-PSDB; ABO33635.

Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 that modulate glucose or free fatty acid uptake by skeletal muscle cells, and are useful for treating diabetes, hyper- or hypo-DB 8; Length 1091 100.0%; Score 1091; DB 8; Length 100.0%; Pred. No. 1.5e-247; iive 0; Mismatches 0; Indels

CK;

0 120 120 180 09 0.9 ACAGGGAAAGGGTGACCTCTGAGATTCCCCCTGACTTTGGAAGTGACCCACC 61 ACAGGGAAAGGGTGACCTCTGAGATTCCCCTTTTTCCCCCAGACTTTGGAAGTGACCCACC Gaps ., Query Match 100. Best Local Similarity 100. Matches 1091; Conservative Н Н 61 d ð

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    Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnerary; cardiant; antidiabetic; ancrectid; antiarthritid; angiogenesis; cancer; adrenal cortical capillary; endothelial cell growth; wound healing; stimulated T-lymphocyte proliferation; immune response suppression; vascular heart hypertrophy; cardiac insufficiency disorder; vascular endothelial growth factor; inflammation; mononuclear cell; cosinophi; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia; chondrocyte redifferentiation; bone disorder; cartilage disorder;
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Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                           Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;
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P-PSDB; ABO44488.
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tissue typing; chromosome identification; vaccine; gene; ss.
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720 721 GGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGGTCTGTGGGG 780 480 480 540 540 999 360 420 420 360 240 240 300 300 Fong S;
Hillan KJ;
Watanabe CK; 120 120 180 180 9 9 361 GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 121 gocricancenderacanceacorrecaecracacaracaecracacaracacara ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGGACCGCACGGGGGGG CACGICICAGGGCATCACCACCACCGAACCATCCCGAICTCCCGGAICTGCTCCAG recordancercearcercecarecearecearecarecressare 241 GAGGGGACCCGCGCGCGCGGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCG GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA ACCAGCAGCATICAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACTGC GAGGGCACCAGCCTGCGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGCG ACAGGGAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC 61 ACAGGGAAAGGGTGACCTCTGAGATTCCCCTTTTTCCCCCAGACTTTGGAAGTGACCCACC 121 AIGGGGCTCAGCAICTITITIGCTCCTGTGTGTTCTTGGGCTCAGCCAGCAGCAGCCACCCG 181 AAGAITITICAAIGGCACTGAGTGTGGGCGTAACTCACAGCGGTGGCAGTGGGGCTGTTT Gaps The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I), having at least 80% sequence identity to a sequence Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in preparation of a medicament for treating a condition responsive to P polypeptide, and as therapeutic agents e.g. vaccines. .0 Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, H Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI; Claim 2; Fig 107; S61pp; English. (GETH) GENENTECH INC. WPI; 2003-585292/55. P-PSDB; ABO33512. 661 199 361 421 541 541 109 601 481 481 H 181 241 301 61 8 8 8 qq q 5 A B S QQ g δ à 엄 δ g à Db à qq à 셤 ò

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, Fong S; Hillan KJ; , Watanabe CK; Ferrara N, Gurney AL, ¹ A, Tumas D, L, Eaton DL, F Grimaldi JC, Gu V, Stewart TA, Baker KP, Botstein D, Desnoyers : goo w, Goddard A, Godowski PJ, (Pan J, Paoni NF, Roy MA, Smith Williams PM, Wood Wi, (GETH) GENENTECH INC.

WPI; 2003-555602/52. P-PSDB; ADC18063.

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841 ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCTTAA

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540 540 900 009 999 099 720 780 780 420 480 480 420 300 360 360 o, 120 180 180 240 240 300 120 The invention relates to human PRO polypeptides and the polynucleotides encoding them. The sequences are useful in the preparation of a dedicament for treating a condition responsive to a PRO polypeptide. The polypeptides are useful in a number of functional biological assays, as molecular weight markers for protein electrophoresis and as therapeutic 9 9 TGCCTCAACCTCTCCATCGTCTCCCATGCCACTGCCATGGTGTATCCCGGGAGAATC CCCIGIGGACAAGAIGGCAICCCTGGAGICIACAACTAIATITGCAAGTATGTGGACTGG ACCAGCACCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC CACGICICAGGCIGGGGCATCACCAACCACGGAACCCAITCCCGGAICIGCICCAG TGCCTCAACCTCTCCATCGTCTCCCATGCCACGTGCTGTGTGTTGTATCCCGGGAGAATC GGGGGCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTTGTGGGG GCCTCGACGAGCCACGACGACGACGCTCCGGCTGCGGCTGCGCCTGCCGTCCGCGTA GCTCACTGCAGCGGCAGCTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCTC GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCCATCCCGGCTACCTGGGA ATGGGGCTCAGCATCTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCACCG AIGGGGCTCAGCAITTTTGCTCCTGTGTGTTTTTGGCTCAGCCAGGCAGCCAACCG AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGGCTTTT GAGGGCACCAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGC GAGGGCACCAGCCTGCTGCGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGG 61 ACAGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAAAGGTGGGGGGGC useful in Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in preparation of a medicament for treating a condition responsive to polypeptide, and as therapeutic agents e.g. vaccines. 0; Length 1091; Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Claim 2; SEQ ID NO 193; 555pp; English 481 109 721 721 781 421 481 541 541 601 661 661 181 241 301 361 361 421 121 181 241 301 121 Н Н 8 6 8 6 2000年 д Б 정 à g 임 qq g à g δ qq õ P ò d $\stackrel{>}{\circ}$ $\overset{\circ}{\circ}$ à

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 961 ACTOTTGTTGGCGTGGGAACTTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA 1020
                                                                         Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis, wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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Fong S; Hillan KJ; Watanabe C Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;

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WPI; 2003-874602/81. P-PSDB; ADD70709.

Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle cells and are useful for treating diabetes or hyper- or hypo-insulinemia.

961 ACTCTIGIIGGCCIGGGAACTICIIGGAACTIIAACTCCIGCCAGCCCTTCTAAGACCCA 1020 ö 900 480 480 540 540 600 009 099 099 720 720 780 780 420 420 360 360 300 300 120 120 180 180 240 240 09 9 CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTTCCCCTAGCTCC 361 GACTGCACCGAGAGAGAGACGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA GGGGGCCCCTGGTGTGTGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGGG CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG ATCCGGATGATCATGAGGAACAGACTGACTGTTTCCTCCACCTCCACCCCCACCCTTAA GAGGGCACCAGCCTGGGCTGCGGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGG GCTCACTGCAGCGGCAGCAGCTACTCGGGTGCGCCTGGGGGAACACACCCTCAGCCTCAGCCACAGCTC GCCTCGACGAGCCACGAGCACGACCTCCGGCTGCGGCTGCGCCTTGCCCCGTCCGCGTA ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC CACGICICAGGCGATCACCAACCACCACGGAACCCATICCCGGAICTGCTCCAG GACTGGACCGAGCAGAGCACAGCGGCTTCTCTGTGACCCCATCCCGGCTACCTGGGA ACAGGGAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC GAGGGCACCAGCCTGCGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCG AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAAGTGGGGCTGTTT . The invention relates to an isolated PRO polypeptide (secreted Length 1091; Indels Query Match
100.0%; Score 1091; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Claim 2; SEQ ID NO 193; 553pp; English. 841 901 901 481 481 541 541 601 601 199 661 721 721 781 781 841 421 Н 61 181 241 241 301 301 361 Н 61 d Op 8 8 8 원 상 원 정염 à ð 8 P & à g à g à 셤 ò gg ð Dp à d à 셤 δ 셤

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                                  961 ACTCTTGTTGGCCTGGGGAACTTCTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA 1020
                         Fong S;
Hillan KJ;
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                                                                                                                                                               Human cDNA encoding secreted/transmembrane protein PRO1303
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Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gu:
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA,
Williams PM, Wood WI;
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The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence dentity con am amino acid sequence chosen from 123 fully defined sequences as contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact o
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New secreted and transmembrane PRO polypeptides useful for treating cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyperhypo-insulinemia, sports injuries and arthritis.
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Best Local Similarity 100.0%; Score 1091; DB 9; Length 1091;
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Indels 0;
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                              ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACGCTGGCACCGATGC
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PR 18-NOV-1999; 99US-014303P.
PR 18-NOV-1999; 99US-014303P.
PR 18-NOS-000; 2000MO-US003P.
PR 18-NOS-
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100.0%; Score 1091; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0;
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17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023522.
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01-JUN-2001; 2010WO-US019692.
29-JUN-2001; 2010WO-US019692.
29-JUN-2001; 2010WO-US01966.
09-JUN-2001; 2010WO-US01166.
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P-PSDB; ADD70232.
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                                                                                                                                               Human cDNA encoding secreted/transmembrane protein PRO1303.
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Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0; Indels
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28-FEB-2001; 2001WO-US006520.

01-WAR-2001; 2001WO-US006666.

01-UJN-2001; 2001WO-US017800.

20-UJN-2001; 2001WO-US019692.

29-UJN-2001; 2001WO-US021066.

09-UJU-2001; 2001WO-US021735.

04-SEP-2001; 2001US-00946374.
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Gao W, Goddard A, Godowski
Pan J, Paoni NF, Roy MA, S
Williams PM, Wood WI;
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P-PSDB; ADD38353.
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Fong S; Hillan KJ; Watanabe CK; Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI; (GETH) GENENTECH INC.

840 ATCCGGATGATCATGAGGAACAGGACCTGTTTCCTCCACCTCCACCCCCACCCCTTAA 900 540 900 900 99 999 720 720 780 780 o, 360 360 420 420 480 480 180 180 240 240 300 300 120 120 09 9 New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773, PRO1244, PRO1246, useful for treating cancerous tumors, cardiac insufficiency disorders, wound healing, Crohn's disease, celiac disease. CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG GCTCACTGCAGCAGCAGCTACTGGGTGCGCCTGGGGGAACACACAGCCTCAGCTTC GACTGGACCGAGGAGATCCGGCACAGCGGCTTCTCTGTGAGACCCATCCCGGCTACCTGGGA ACCAGCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGGCACCGAGTGC CACGICTCAGGCTGGGGCATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCAG GGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGG CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG GAGGGCACCAGCCTGCGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCG GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC CACGICICAGGCATCACCACCACCACGGAACCCAIICCCGGAICTGCTCCAG AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGGCTGTTT 241 GAGGGCACCAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGCG ACAGGGAAAGGGGGCCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC Gaps Ö 0; The invention relates to an isolated PRO polypeptide (secreted DB 9; Length 1091; 0; Indels 100.0%; Score 1091; DB 9; 100.0%; Pred. No. 1.5e-247; iive 0; Mismatches 0; Claim 2; SEQ ID NO 193; 555pp; English. Best Local Similarity 100. Matches 1091; Conservative WPI; 2003-765477/72. P-PSDB; ADD38832. 301 199 181 841 361 421 421 481 481 541 541 601 601 199 721 721 781 61 61 181 241 Query Match Best Local (ò 셤 ò g à qq g ठे Op δ g П g δ qq δ 8 αq q ò g δ à g δ à ద à

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                                                                       841 ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCCTTAA 900
                                                                                                                                                                                                                                                                                           Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diables; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
                                                                                                              CTIGGGIACCCCTCIGGCCCTCAGAGCACCAAIAICTCCTCCATCACTTCCCCTAGCTCC
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CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCC

The invention relates to an isolated PRO polypeptide (secreted

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Query Match
100.0%; Score 1091; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.5e-247;
Matches 1091; Conservative 0; Mismatches 0;

121 AIGGGGCTCAGCAICTTTITGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACCG

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Watanabe CK;
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01-DEC-2000; 2000WO-US03328.
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01-DEC-2000; 2000WO-US03673.
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04-SEP-2001; 2001WO-US011066.
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Gao W, Goddard A, Godowski
Pan J, Paoni NF, Roy MA, S
Williams PM, Wood WI;
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P-PSDB; ADD40263.
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181 AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCCTGTTT

ACTCTIGTIGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA 1020 CTIGGGIACCCTICGGCCCTCAGAGCACCAATAICTCCTCCATCACTICCCCTAGCTCC 960 CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTACCTCTAGCTCC GGGGGCCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCTCTGGGGGTTCTGTGGGGG GGGGCCCCCTGGTGTGTGGGGGGGTCCTTCAAGGTCTGGTGTGCTGGGGGTCTGTGGGG CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCTTAA 961 841 901 901 199 721 721 781 781 841 gg 쉽 ö g ò g à ò g 8 New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773, PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac insufficiency disorders.

Claim 2; SEQ ID NO 193; 550pp; English

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Search completed: June 20, 2004, 02:29:02 Job time : 514 secs

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Mus musculus adult male tongue CDNA, RIKEN full-length enriched library, clone:2310008B01 product:similar to KALLIKREIN 12 PRECURSOR (EC 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) [Homo sapiens], full insert sequence.

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AK009217
HTC; CAP France.
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CD503320 CDA61-F06
CD501456 CDA50-H11
CD505738 CDA75-D03
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CDA61-F06
CDA61-F06
                                                                                       AK009720 Mus muscu
AY410899 Pan trog1
AY410890 Mus muscu
CB202840 AGENCOURT
AY410898 Homo sapi
AK009559 Mus muscu
CB587168 AGENCOURT
BI763040 603047836
CB574882 AGENCOURT
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CDA96-G05
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                 A1324852 mi20d11.x
AA028356 mi20d11.r
A1322408 mi20d11.y
BC035385 Homo sapi
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                   W20715 mb93f12.rl
BG230967 nag78a04.
BC015551 Homo sapi
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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CB587168
BI763040
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                  /note="unnamed protein product; putative similar to KALLIKREIN 12 PRECURSOR (EC 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) [Homo sapiens] (SWISSPOT)[Q9UKRO, evidence: FASTY, 70.6%ID, 94.7%length,
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

( (Dases I to 890)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
                                                                              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishiner, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Murametsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Generol pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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/db_xref="FANTOM_DB:2310008B01"
/db_xref="MGI:1901647"
/db_xref="taxon:10090"
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence Clustering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="RIKEN full-length enriched, adult male tongue"/note="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp,

dachi,J., Aizawa,K., Akimura,T., Farakawa,T., Carninci,P.,

Rudachi,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,

Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,

Imotani,K., Numazaki,R., Ohno,M., Ohsaki,A., Murata,M., Nakamura,M.,

Nomura,K., Numazaki,R., Ohno,M., Ohsako,Ohno,W., Osato,R., Sakazume,N.,

Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,

Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 472)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

Radelof,U., Schneider,D. and Korn,B.

Human Unigneset - RZPD3

Contact: Ina Rolfs
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RZPD118; I.M.A.G. E. CDNA Clone Collection; Human UnigeneSet - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/Ogi-brtp;/kwww.rzpd.de/CloneCards/Ogi-brtp;/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: 449 30 32639 101 Fax: 449 30 32639 111 www.rzpd.de
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|mol_trype="mRNA"
|AD_xref="taxon:9506"
|clone="IMAGE:2109677"
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Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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469 bp mRNA linear EST 30-MAR-1999
tg24b33.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109677 3'
similar to SW:TRY3 CHICK Q90629 TRYPSINOGEN 2-P29 PRECURSOR.
;contains TAR1.bl TAR1 repetitive element ;, mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 469)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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ttissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
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99.7%; Pred. No. 6.4e-62;
tive 0; Mismatches 1;
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Unpublished (1997)
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Best Local Similarity 99.73
Matches 375; Conservative
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us-10-015-385a-193.rst

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UI-R-CN1-cmq-p-20-0-UI.sl UI-R-CN1 Rattus norvegicus CDNA clone
UI-R-CN1-cmq-p-20-0-UI 3', mRNA sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                          Query Match 28.6%; Score 311.8; DB 9; Length 469; Best Local Similarity 97.3%; Pred. No. 9e-50; Matches 328; Conservative 0; Mismatches 7; Indels 2;
found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1051 Std Error: 0.00
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                                                                                                                           organism="Homo sapiens"
                                                                      stop: 397.
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                                     Insert Length: 1051 Std Brr
Seq primer: -400P from Gibco
High quality sequence stop: 3
Location/Qualifiers
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                                                                                                                                                                                                                                       The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand oDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized fundus library oDNA Library Preparation: M.B. Soares Lab Genetics (www.resgen.com)
                                                                                                             USA
                                                        University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, TE1: 319 335 8250 Fax: 319 335 9565
                                Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UI-R-CN1-cmq-p-20-0-UI"
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/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db xref="taxon:10116"
                                                                                                                                                                                                                       Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Forward
POLYA=Yes.
Contact: Soares, MB
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R-CVO-BRH through R-CVO-BRR, R-CVI-BRS through R-CVI-BSC, R-CVI-BSC, EvCVI-BSC through R-CVI-BSC, and R-CVI-BSC through R-CVI-BSC.

R-CVI-BVU. This pool represented about 54 of the final driver population. e) A pool of about 10,000 clones from subtracted library BSC, BVO and BVOP (7-9.5 kb CDNA library fraction from rat whole embryo), and BXO (0.5-7kb cDNA library fraction from rat whole embryo), and BXO (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to places R-BS_B-BBS kbrough R-BSC-BFB, R-BVO-ANK through R-BVO-ANK, R-BVO-ANK, Through R-BYO-ANK, Through R-BYO-ANK, Through R-BYO-ANK, Through R-BYO-ANK, Through R-BYO-ANK, Through R-BYO-ANK, Through R-BYO-BYO, DDO, DDO, and DEO corresponding to places R-CXO-BFP, F-BNO-BZ, R-CZO-BYO, Through R-DBO-BZA, R-CZO-BZD, Through R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-CAA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-DBO-BZA, R-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local
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/clone lib="Scares mouse p3NMF19.5"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo (dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 25-JUN-2003
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus.
I (bases 1 to 520)
Hell,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
and Korn,B.
                                                                         315
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contact RZPD (clone@rzpd.de) for further information. Seg primer:
T7, Primer sequence: TAATACGACTCACTATAGGG.
Location/Qualifiers
1. .520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     878 CCACCTCCACCCCACCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCT
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                                                                                                                                                                                                 TGGTGTCCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCT
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BX514743 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGP9998N221098 ; IMAGE:464085, mRNA sequence.
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH108 (ampicillin resistant)"
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., La, M., Martin, J., Morris, M., Schellenberg, K., Steptco, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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               double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                  61
A1324852 545 bp mRNA linear EST 23-DEC mi20411.x1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE.464085 3' similar to SW:TRY1_CHICK Q90627 TRYPSINOGEN PRECURSOR. ; mRNA sequence.
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Pred. No. 3.6e-44;
0; Mismatches 139; Indels
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
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                                                                                                                                                only, this new
                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                5' end
                                                                                                                           MOI:277901
This clone was previously sequenced on the data is from the 3' end
High quality sequence stop: 475.
Location/Qualifiers
             Washington University School of MedicineP
                                                                                                                                                                                                                                 organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:464085"
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WashU-HHMI Mouse EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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                                                                                                                            AA028356 506 bp mRNA linear EST 11-SEP-1996 mi20d11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:464085 5' similar to SW:TRYP_BOVIN P00760 TRYPSINOGEN ;, mRNA
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Marra, M., Hillier, L., Aller, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:277901
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Washl-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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High quality sequence stop: 486
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 449)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterstonn,R. The WashU-HMNI Mouse EST Project
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mi20d11.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:464085 5' similar to SW:TRY3_SALSA P35033 TRYPSINOGEN III
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                GAAGCCGGGAAGGATGCCTGTCAGGGTGACTCTGGAGGCCCCCTGGTGTGGAGGGGTT
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/mol type="mRNA"

Mol xref="taxon:10090"
/clone="IMAGE:464085"
/dev_stage="19.5 dpc total fetus"
/lab_nost="DH10B (ampicillin resistant)"
/clone lib="Soares mouse p3NR19.5"
/note="Vector: pT773D (Pharmacia) with a modified
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GAGACGTGCCGGCTGTGTTTCCTGGAAGAGTGACGGAGAATATGTTGTGCAGGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CTTCAAGGTCTGGTTTCCTGGGGATCTGTTGGGCCTTGTGGGTCAAAAAGGTATTCCAGGA
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0
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                                                                                                                                                                                                                                                                                                                                                                                                         23.6%; Score 257.2; DB 9; Length 74.0%; Pred. No. 2.8e-39; ive 0; Mismatches 114; Indels
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Contact: MGC help desk
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1 (bases 1 to 1186)
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Direct Submission
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391 bp mRNA linear EST 10-SEP-1996
mb93f12.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:337007 5' similar to SW:TRYP_BOVIN P00760 TRYPSINOGEN ;, mRNA
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 817
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637
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                                                                                                                                                                       Η.,
                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 71 Row: m Column: 9 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802 ACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 AGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGAGTCCTTCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTGTCCTGGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 ATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAGGCGGCGCGTCCCGGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 ACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCC
                                                                                                                                                                          Loulseged,
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cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.0%; Score 250.4; DB 11; Length 1186; 99.6%; Pred. No. 5.2e-38; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/note="Vector: pBluescript"
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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4825490"
/tissue type="Testis"
/clone_lib="NIH_MGC_97"
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Best Local Similarity 99.6
Matches 251; Conservative
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Homo sapiens (human)
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BC015551
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Washington University School of Medicine?
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
Inix Clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:218407
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/db_xref="taxon:10090"
/clone="IMAGE:337007"
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Best Local Similarity 74.5%;
Matches 292; Conservative (
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BG230967 2. NCI CGAP HN8 Homo sapiens cDNA clone IMAGE:4227367 similar to TR:Q9UKRI Q9UKRI KALLIKREIN-LIKE PROTEIN 5-RELATED BG230967 ;, mRNA sequence.

LOCUS

BG230967

BG230967.1 GI:12726030

ACCESSION

VERSION

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Edward Shllittoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 264)
                                                               1 (bases 1 to 264)
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NOI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute / National Institute of Dental Research.
Cancer Genome Austomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pAMP10; cDNA made by oligo-dT priming.
Non-directionally cloned into the UnG sites of pAMP10.
Size-selected on agarose gel, average insert size 500 Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
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/tissue type="well-differentiated invasive carcinoma, floor of mouth"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1037 AGTGTGCAATAGTCTGGAATAAATAAATGAAGGA 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%; Score 216; DB 12;
100.0%; Pred. No. 2.4e-31;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AGIGIGCAATAGICIGGAATAAATAAATGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           info@image.llnl.gov
Seg primer: -40UP from Gibco
High quality sequence stop: 257.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               errors.
BC015551
BC015551.2 GI:34190438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 216; Conservative
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KEYWORDS
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440 414 468 560 588

680

528 620 648

705 800 765 860 825 882 977

917

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK009360 1295 bp mRNA linear HTC 20-SEP-2003 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                          CAGCCCACTGCCTCAAGCCGTGGCCGCTACATAGTTCACCTGGGGCAGGACAACCTCCAG
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                                                    299 CGGCTCACTGC----AGCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGC
                                                                                                                                                                                                                                                                 441 AAGGAGGAGGCTGTGAGCAGACCGGACAGCCACTGAGTCCTTCCCCCCACCCGGCTTC
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                                                                                                                                                                                             355 CAGCTCGACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTAC
                                                                                                                                                                                                                                                                                                                                       CTGGGAGCCTCGACGAGCACGACCAC-----GACCTCCGGCTGCGGCTGCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                          501 AACAACAGCCTCCCCAACAAGACCACCGCAATGACATCATGCTGGTGAAGATGGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 GATCTGCTCCAGTGCCTCAACCTCCCATCGTCTCCCATGCCACCTGCCATGGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGAGTCCTTCAAGGTCTGGTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 CCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCCTCTCCTCACGCTGTGTCACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGGGAGAATCACGAGCAACATGGTGTGTGCAGGCG---GCGTCCCGGGGGCAGGATGCC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK009360.1 GI:12844110
HTC; CAP trapper.
Mus musculus (house mouse)
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AUTHORS
TITLE
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PUBMED
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KEYWORDS
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenco, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McWan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Gardia, A.M., Madan, A., Rodrigues, S.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X. (Sibbs, R.A.,
Banker, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lint at: http://image.llnl.gov Series: IRAK Plate: 20 Row: i Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21618356 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA 94305
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Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Genome
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On Aug 25, 2003 this sequence version replaced gi:15930236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/tissue type="Colon, adenocarcinoma"
/clone lib="NIH MGC_65"
/lab host="DH108"
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llarity 59.1%; Pred. No. 6.1e
Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Aug 25, 2003 this sequence
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: ATCC
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/translation="MRRLKSDWKLSTETREPGARPALLQARMILRLIALALVTGHVGG
ETRIIKGYECRPHSQPWQVALPQKTRLLCGATLIAPKWLLTAAHCRKPHYVILLGEHN
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CAAAGTSCLISGWGTTSSPQLALPHSLRCAAVSIIBHKECRKAYPGNITDTMLCASVR
KEGKDSCQGDSGGPLVCNGSLQGIISWGQDPCAVTRKPGVTKVCKYFNWIHEVWRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGAAGACACGGCTTCTCTGTGGGGCAACCCTCATCGCCCCCAAATGGCTCCTGACAG
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                          /note="unnamed protein product; protease, serine, (MGD|MGI:1929977)
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                                                                                                                                 /protein_id="BAB26241.2"
/db_xref="GI:26364453"
                                                                                                                                                                                                                                                                                                                                                                                                               /note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-reseges.riken.go.jp, URL:http://genome.ges.riken.go.jp, Tel:81-45-503-922, Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
144. _974
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1295)
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                                                                                                                                                                                                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
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db_xref="MGI:1894001"
db_xref="taxon:10090"
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|strain="C57BL/6J"
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LEKTDGCEQRRMATESFPHPDFNNSLPNKDHRNDIMLVKMSSPVFFTRAVQPLTLSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="tongue"
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KEGKDSCQGDSGGPLVCNGSLQGIISWGQDPCAVTRKPGVYTKVCKYFNWIHEVMRNN
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             Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwadi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-1384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                AK009720
Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1295)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                    700 CCTTGCGATGTGCCAATGTCTCCATCATCGAAGAAGAAGTGTGAGAAGGCCTACCGG 759
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593 IGCICCAGIGCCICAACCICICCAICGICTCCCAIGCCACCIGCCAIGGIGIATCCCG 652
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TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 139
LENGTH: 619
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ACCAATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGG
                                                    AGCCGTGGCAGGTGGGGCTGTTTGAGGGCACCAGCCTGCGGCTGCGGGGTGTCCTTATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: trypsin-like serine proteases US-09-280-116-139
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Patent No. 6331427
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-280-116-139
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APPLICANT: YOURS OF THE STREAM INCOMMATION:
APPLICANT: YOUNG et al.
TITLE CR INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007D1
FILE REFERENCE: P2007D1
FILE REPERENCE: P2007D1
FILE REPERENCE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER APPLICATION NUMBER: 60/048,881
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EARLIER FILING DATE: 1997-06-06
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EARLIER FIL
Sequence 247, Application US/09205258 Patent No. 6525174
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APPLICANT: COHEN, MAURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: FRIEDRAM, PAULA N.
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWERL, JOHN C.
APPLICANT: STEWERL, STEVEN D.
APPLICANT: STEWERL, STEVEN D.
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISBASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                        641
                                                                                                                                                                                                     528 CCTGCCTCACACCTTGSGATGCGCCAACATCACCATCATTGAGGACGCAGAAGTGTGAGAA 587
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408 GGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCCTCTCCTCACGCTGTGT 467
                                                                                                                                                                   582 ATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGG
                                                                                                                                                                                                                                                                                                                          765 AGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCAC
                                                          468 CACTGCTGGCACCAGCTGYCTCATTTCCGGCTGGGGCAGMACGTCCAGCCCCCAGTTACG
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                                                                                                                                                                                                                                                                              ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEREQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCTCCACCCCCACCCCTTAACTT 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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PAPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 GCTCCTGACAGCAGCCGACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGGGGAGCAGAA 287
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                 EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER APPLICATION NUMBER: 60/048,898
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EARLIER APPLICATION NUMBER: 60/048,963
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EARLIER APPLICATION NUMBER: 60/048,877
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EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-07-15
EARLIER FILING DATE: 1997-07-15
EARLIER FILING DATE: 1998-07-15
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OTHER INFORMATION: n equals a,t,g, or c
0.9-205-258-247
  1997-06-06
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OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (35)
OTHER INFORMATION: n equals
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Best Local Similarity 58.5
Matches 436; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (36)
OTHER INFORMATION:
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LENGTH: 1146
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TRACEY L.
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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59.0%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 433; Conservative
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                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                        APPLICANT: KLASS, MICA APPLICANT: RUSSELL, JG APPLICANT: STEWART, KE APPLICANT: STRONDE, STITLE OF INVENTION: NO TITLE OF INVENTION: APPLICANT OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                CLLL
STATE: LL
COUNTRY: USA
TTD: 60064-3500
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                      Length 1166;
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                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                        1, Mismatches 289;
                                                                                                                                                                                                                                                                      Score 217.8; DE
Pred. No. 2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCCTCGACGAGCCACGAGCAC-
                                            INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1166 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                      20.0%;
58.9%;
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  847/938-2623
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Best Local Similarity
Matches 432; Conserv
     TELEFAX:
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RESULT 5
US-09-44-83-8
iSequence 8, Application US/08944483
; Sequence No. 6232456
; Patent No. 6232456
; GENERAL INFORMATION:
abplicant: COHEN, MAURICE

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ERIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
VENTION: NOVEL SERINE PROTEASE REAGENTS
VENTION: OF THE PROSTATE
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Pred. No. 2.3e-50;
0; Mismatches 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
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CATCACCCTCCATT 1012
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TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: LUNGTUT10 CLONE: 2723646
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US-09-025-059-2
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
CORRESPONDENCE ADDRESS:
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SOFTWARE: FESESEG OF Windows Version 2.0
CURRENY EPELICATION DATA:
APPLICATION NUMBER: US/09/025,059
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STREET: 3174 Porter Dr.
CITY: Palo Alto
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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Patent No. 6075136
GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,749
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SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Disket
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STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                    <u>CAGCCACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAAACCTCCAGAAGG</u>
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Length 1314;
   19.9%; Score 217.6; DB 3; 59.0%; Pred. No. 2.4e-50;
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Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
                                                                        0; Mismatches
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æ. 592 298 444 418 472 564 624 652 744 709 804 769 829 921 889 324 504 684 864 981 AGGAGGCTGTGAGCAGACCGGACAGCCACTGAGTCCTTCCCCCACCCCGGCTTCAACA cerricioariciocarcarcarcaricarioageaceacadasericioaraceceracece 922 ATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCACACAGSC TTGAGGGCACCAGCCTGCGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAG rcandanda cecescina circi en escaca con contra con contra c cadeceacridecercaageeecederacaractricaceridegeeaceacaaacerecagaage 359 TCGACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCCATCCCGGCTACCTGG GAGCCTCGACGAGCCACGAGCAC----GACCTCCGGCTGCTGCGGCTGCGCCTGCCCG ACAGCCTCCCCAACAAGACCACCGCAATGACATCATGCTGCTGGAAGATGGCATCGCCAG TCCGCGTAACCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCA rencearcacheschengeskedeerereacereneerereaceriereneachengen TGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTATCCCG GGAGAATCACGAGCAACATGGTGTGTGTGCAGGCG----GCGTCCCGGGGCAGGATGCCTGCC AGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGG AGGGTGACTCCGGGGGCCCTCTGGTAACCAGTCTCTTCAAGGCATTATCTCCTGGG GGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGT G---ccaddarccererecearceceaaaccredrereracacaaagrerecaaar ATGIGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCC CGAAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGGCTGT ccaedarcarcaadegerrceadrecaadecreacheceadeceredeadecadecerer 12; Length 1292; DB 4; Score 216.8; DB 4; Pred. No. 3.9e-50; 2; Mismatches 289; EARLIER FILING DATE: 1997-06-06
BARLIER APPLICATION NUMBER: 60/070,923
BEARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 189 2; 19.9%; ilarity 58.7%; Conservative 2 CCACCCTTAACTT 903 CATCACCTCCATT 995 ORGANISM: Homo sapiens US-09-205-258-189 Similarity 431; 710 179 325 299 385 565 685 982 265 239 445 419 473 533 625 593 653 745 805 770 865 830 890 Query Match Best Local g qq d ò g d qq δ Db δ g à d à ò qq à ò ò ò à g à ð Dp

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                                                                                                                                                                                                                                                         654 GAGAATCACGAGCAACATGGTGTGTGCAGGCG---GCGTCCCGGGGGCAGGATGCCTGCCA 710
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594 GCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTGTATCCCGG 653
                                                                                                                                                                                                                                                                                         CAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGGAAGGGGCAAGGACTCCTGCCA 634
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                                               CGAGTGCCACGTCTCAGGCTGGGGCATCACCAACCACCGCACGGAACCCATTCCCGGATCT
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APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Cymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT APPLICATION NUMBER: US/09/386,642
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
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Matches 395; Conserva
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LENGTH: 1052
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                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
TITLE OF INVENTION: RALLIKREIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskerte
COMPUTER: 1BM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
                                                                                                                                                                                       STREET: 3174 Porter Drive CUTY: Palo Alto CUTY: CA
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NAME: Billings, Lucy J.
REGISTATION UNDERER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELEFONN: 12-85-0555
TELEFAX: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                     Sequence 2, Application US/08790137
Patent No. 5840871
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.6%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-790-137-2
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277 GACCACAGGIGGGICCICACAGCGGCICACIGCAGCGGCAGCAGGIACIGGGIGCGCCIG 336
814 ACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAA 863
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APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TILLE OF INVENTOR: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGAICATAGGCAGCAA 53
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Pred. No. 3.6e-43;
0; Mismatches 304; Indels
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CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/09618259; Patent No. 6642013
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Best Local Similarity 56.3%;
Matches 400; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCTCATTTCCGGCTGGGCAGCACGT
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                                                                                          TGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGGCATCACCA
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                                                                                                                                                                                                                                     ATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAGGCG
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                   TCCGGCTGCTGCGGCCTGCCCTGCCCGTCCGCGTAACCAGCGTTCAACCCCTGCCCC
                                                                                                                                                                                                   557 CCAGCCCCAGTTACGCCTGCCTCACACTTGCGATGCGCCAACATCACATCATTGAGC
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APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 72
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56.3%; Pred. No. 3.6e-43;
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Best Local Similarity 56.3
Matches 400; Conservative
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US-09-618-259-72/c
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157 GGGCTCAGCCAGGCGACACCGAAGATTTTCAATGGCACTGAGTGTGGGCGGTAACTCA 216
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Pred. No. 8.7e-43;
0; Mismatches 305; Indels
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                     REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-09-008-271A-19
   NAME: Mohan-Peterson, Sheela
                                                                    TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.2%;
Matches 399; Conservative
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CLONE: 1798496
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US-09-386-642-9
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GGGGAACACACGCCTCAGCCAGCTCGACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCT 396
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COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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STREET: 3174 Porter Dr.
CITY: Palo Alto
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APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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57.4%; Pred. No. 2.5e-42;
Live 0; Mismatches 276;
                                                                                                                                                                                                        APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT APPLICATION NUMBER: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
Sequence 9, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
Sequence 1, Application US/09070526
Patent No. 6100059
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: GLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: No. 6100059el Compounds
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-07W-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1197
ATTOGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
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Best Local Similarity 55.6
Matches 395; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCGTTCAACCCCTGCCCTGCCCAAT
                                                                                     GACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGCATCACCACCACCAC
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US-08-467-155A-2
US-08-467-155A-2
Sequence 2, Application US/08467155A
PARTENE NO. 5736377
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DN
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
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ATTOKNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100001
TELECHOMUNICATION INFORMATION:
TELEPHONE: 617/542-6070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,155A
FILING DATE: 06-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENČE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALL STREET: 22.
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TOPOLOGY: lir
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Score 173.8; DB 1; Length 1454; Pred. No. 3.1e-38;

15.9%; 56.3%;

Query Match Best Local Similarity

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    Indels
Mismatches 287;
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    Conservative
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Job time: 101 secs
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID 1091 100.0 1091 6 AXE 1091 100.0 1091 6 AXE 1091 100.0 1091 6 AXE 440 40.3 840 6 AXE 440	SUMMARIES Description	nordinased		AA69/125 Sequence	AISSOSZĘ BX648580	AR263961 Sequence	AR337568	BD130047	AF164623	AF135025 AC011473	AF243527	AC073185	AX070938 Seq.	AC140096 Fan AC130782 Pan	AC073185 HOMC		AB100393 AX697374	AX697375	Z Continual	AC027113	AC099756	AC025349 AT.844197	APOOSSOL	AC135541	AC127853	G78591 S209P619	AX375740 Sequence	AX375744 Seguenc	X04036 S	E00424 Pig elast	AX823454 DR2546996	AX676264 Sequenc	AR256990 Sequer	Arssessa nomo s BC062334 Homo s	BC036846 Homo s	Continuation (2		ALIGNMENTS		יייסתיון אועם	ineat FAI 02-AFR-20			Craniata; Vertebrata	Catarrhini; Hominidae; Homo.	Williams, P.M., Baker, K.P., Desnoyers, L.,
AX697125 AX6	Ħ	- ;	:																																			ALIG		1001	7	m	(q	•		A., W.
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	AY358524 Non Homo sapiens clone DNA65409 KLK12 (UNQ669) mRNA, complete cds. AY358524 AY358524. GI:37182170 FLI CDNA. Homo sapiens (human) SM Homo sapiens (human) SM Homo sapiens Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mararyota; Metazoa; Chordata; Craniata; Catarrhini; Hominidae; Homo. E I (bases I to 1091) S Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Kilm,H.S., Kilm,H.S., Lilmowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,	Schoelled, J., Senagari, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagre, A., Vadre, A., Vandlen, R., Watanabe, C., Wiead, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Zhang, M.,	11091 Alocus tag="UNQ669" Alocus tag="UNQ669" Alocus tag="UNQ669" Alocus tag="UNQ669" Alocus tag="Tag="13" Alocus tag="13
8 8 8 8 8 8 8	RESULT 2 AY35854 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE ANTHORS TITLE JOURNAL FEATURES	CDS
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K. the same JOURNAL Patent: Wo 0078961-A 193 28-DEC-2000; FRATURES Genetech Inc. (US) Genetech Inc. (US) Genetech Inc. (US) L. 1091 And Ltype="unassigned DNA" Ouery Match: Best Local Similarity 100.0%; Score 1091; DB 6; Length 1091; Best Local Similarity 100.0%; Pred. No. 0; Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0; L. AAGCAGGTCATCCCCTTGAGGACACACAGAGGGCAGAGGGGGGGC 60 L. CAAGCAGGTCATCCCCTTGAGGACACACAGAGGGCAGAGGGGGGGC 60		301 361 421 481 481 541 601	DD 601 TGCTCAACCTCTCCATCCTCCCATGCTCTCCATGCTATCCCGGGGAAATC 600 661 ACGAGCAACATGGTGTGTGTGTGTGTGTGTGTGTGTGTGT

	RESULT 3 HSM808731 LOCUS DEFINITION Home sapiens mRNA; cDNA DKFZp686H1078 (from clone DKFZp686H1078). ACCESSION BX648580.1 GI:34367742 KEYWORDS	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REPERENCE 1 (bases 1 to 811)		Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany within the cDNA sequencing consortium of the German Genome Project.	This clone (DKFZp686H1078) is available at the RZPD in Berlin. Please context the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available	at http://mips.gsf.de/proj/cDNA/. FEATURES Location/Qualifiers source 1811 /organism="Homo sapiens"	/mol_type="mRNA" /db_xxef="haxon:9606" /clone="DKF2p686H1078" /tissue_type="human endometrium carcinoma cell line"	/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfiIA + SfiIB" /dev_stage="adult" polyA_signal 702707		Best Local Similarity 100.0%; Pred. No. 1.4e-284; Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 578 ACCCATTCCGGATCTGCTCCAGTGCCTCAACCTCTCCATGGTCTCCCATGCCACGTGCC 637		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	346 AGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTC	VY 758 1951GITCITGGGGGTCITGITGGGACAAGATGGCATCCCTGGAGTCTACACT 817	466 ATATTIGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCT
Query Match 100.0%; Score 1091; DB 9; Length 1091; Best Local Similarity 100.0%; No. 0; No. 0; Atches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CAAGCAGGTCATCCCTTGGTGACCTTCAAAGGAAGCAGAAGGAAG	Oy 61 ACAGGAAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTGGAAGTGACCCACC 120 Db 61 ACAGGGAAAGGGTCACCTCTGAGATTCCCCCTTTTCCCCCCAGACTTTGGAAGTGACCCACC 120 Qy 121 ATGGGGTCAGCATCTTTTGCTCTGTGTTTCTTGGCTCAGCCAGGCACCACCC 180 Db 121 ATGGGGTCAGCATCTTTTTGCTCCTGTGTTTCTTGGGCTCAGCCACCCAC	81 AAGATTTTCAATGGCACTGAGTGTGGGGGGTAACTCACAGCCGTGGCAGGGGGGTGTTT 	Qy 241 dAGGGCACCAGCCTGCGGGGGGTGTCCTTATTGACCACGGTCCTCACAGGG 301 GAGGCACCAGCCTGCGGGGGTGTCCTTATTGACCACGGTCCTCACAGGGGGG 301 GCTCACTGCGGCTGCGGGGGGTGTCCTTATTGACCACGGGGGAACCAGGTCCTCACAGGGGGGGG	OY 361 GACTGGACCAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420 Db 361 GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420	421 GCCTCGACGAGGCACGACGACCTCCGGCTGCTGCGCCTGCCCGTCCGCGTA 480	481 ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACGGAGGG 540	Oy 541 CACGICICAGGCIGGGGAICACCACCACGGAACCCAITCCCGGAICIGCTCCAG 600	601 TGCCTGAACTCCTCCATGCCATGCCACGCCATGGTGTGTATCCCGGGGAGAATC 660 [661 ACGAGCAACATGGTGTGCAGGCGGCGTCCCGGGGAAGATGCCTGCC	721 GGGGGCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCTCGGGGGTCTGTGGGG 780 	781 CCCTGTGGACAAGATGCCATGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG 840 	TTAA TTAA	901 CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTTCCCCTAGGTCC 960	ACTCTTGTTGG 	1021 CGAGCGGGGTGAGAAGTGTGCAATAGTCTGGAATAAATATAAATGAAGGGGGGCAAA 1080

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  PAT 17-AUG-2003
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Pred. No. 5.7e-250;
0; Mismatches 1; Indels
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BD130047
BD130047.1 GI:23224992
linear
                                                                                                                                                                                    (Asses 1 to 840)
Ni,J. and Ruben,S.M.
Human serine protease and serpin polypeptides
Patent: US 656498-A 5 20-MAY-2003;
Location/Qualifiers
  DNA
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                                                  PRI 26-JUN-2000
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1 (Joses 1 to 9120)

Yousef, G.M., Scorilas, A. and Diamandis, B.P.

Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human Xallikrein gene family

Genomics 63 (1), 88-96 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Yousef, G.M., Scorilas, A. and Diamandis, E.P.
Direct Submission
Submitted (01-UUL-1999) Pathology and Laboratory Medicine, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario MSG 1x5,
                                            AF164623 9120 bp DNA linear PRI 26-JUN-2
Homo sapiens trypsin-like serine protease (TLSP) gene, complete
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2313. 7622
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join(2313. 2399,4189. 4263,5061. .5217,5545.
/gene="TLSP"
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oin(4224. .4263,5061. .5217,5545. .5810,6627.
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100.0%; Pred. No. 3.4e-208;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="19"
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AF164623.1 GI:5713130
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gene="TLSP"
                                                                                                                                                                  Homo sapiens (human)
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Matches 37
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                                                             DEFINITION
                                                                                                                                                                                     ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                   AUTHORS
TITLE
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AUTHORS
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PUBMED
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    RESULT 7
AF164623
LOCUS
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PN 025502600-A/3
PD 29-JAN 2002
PP 04-FEB-1999 JP 2000530597
PR 06-FEB-1999 US 60/073961
PR 1 STEVEN M RUBEN, JIAN NI
PC CI2N9/64, AGLK38/48, AGLP7/02, AGLP7/04, AGLP7/06, AGLP29/00, AGLP31/PC
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PC C12N5/10,C12N15/09,C12Q1/37,A61K37/547,C12N5/00,C12N15/00 CC
Human serine protease and serpin polypeptide
FH Key Location/Qualifiers
FT CDS
Location/Qualifiers
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 840)

Ruben, S.M. and Ni, J.

Ruben, S.M. and Ni, J.

Human serine profease and serpin polypeptide
Patent: JP 2002502600-3 32-JAN-2002;

HUMAN GENOME SCIENCES INC
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99.8%; Pred. No. 5.7e-250;
tive 0; Mismatches 1; Indels
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JP 2002502600-A/3.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 490; Conserv
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77147847,91789293,94239543) /product="kallikrein-like protein 5-related protein 1" join(37433840,39954050,44964655,77147847, 91789543) /product="kallikrein-like protein 5-related protein 2" join(40144050,44964655,65006759,77147847, 91789293,94239480) /note="KLK-L5-related protein 1; kallikrein-like serine proteesse; alternatively spliced" /codon_starla. /codon_starla. /protein_id="kallikrein-like protein 5-related protein 1" /protein_id="kallikrein-like protein 5-related protein 1"	/ db xref="G1:6249632" / translation="MGLSIPFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTS / translation="MGLSIPFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTS LRCGCVLIPHRWULTAALGSGSRYWWRLGEHSLSQLDWTEOTRHSGFSVTHFCYLGAS TSHEHDLRLIRLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGTTNHPRNPFPDLLQ CLNASIVSHAATCHGYYPGRTTSDNWCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGS VGPGGQDGIPGYTYTCNSTLVGLGTSWNFNSCQPF" join(40144050,44964655,65006759,77147847, 91789333 /note="KIK-L"" / codon_start=1 / product="Kallikrein-like protein 5" / product="kallikrein-like protein 5" / proctin_id="AAD26456.2"	/ CTAIRSTAIL OF 1912 1912 1912 1912 1912 1912 1912 191	h Similarity 100.0%; Pred. No. 3.4e-208; 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CCAGGGTATTCTGGGGGCCCCCTGGTGTGTGGGGGGAGTCCTTCAAGGTCTGGTGTCCTG	AACTGACTCTTCCTCCACCTCACACCTCCACACCTCACACCTCTTCCTCC		CTTCTAAGACCCACGAGCGGGGGGGGGAGAAGTGTGCAATAGTCTGGAATAAATA
mrna CDS	CDS	CDS DOJVA Si	. do 1 €	70 170 170 176	223 228 828 Db 9294	935	Db 9474 Qy 1068
948 TTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCC 1007 634 TTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCC 693 1008 CTTCTAAGACCCACGGGGGGGGGGGGGGGGGGGGGGGGG	AF135025 M Homo sapiens kallikrein-like products, complete cds. AF135025 AF135025.2 GI:6166248 Homo sapiens (human) M Homo sapiens (human) Frietrocka. Metazoa Chordata.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo (bases 2909 to 7847) Yousef,G.M., Luo,L. and Diamandis,E.P. Identification of novel human kallikrein-like genes on chaticancer Res. 79 2843-2852 (1999) 2 (bases 1 to 11820) 2 idases 1 to 11820) 2 idases 1 to 11820; Metab. 11 (2), 54-60 (2000) 21121728 3 (bases 1 to 11820) 3 (bases 1 to 11820) 3 (bases 1 to 11820) 3 (bases 1 to 11820) 4 Vousef,G.M., Magklara,A. and Diamandis,E.P. Xusef,G.M., Magklara,A. and Diamandis,E.P. Xusef,G.M., Magklara,A. and Diamandis,E.P. Xik-L5 is a novel serine protease and a new member of the				Sequence update by submitter On Nov 1, 1999 this sequence version replaced gi:4589276. Location/Qualifiers 1. 11820 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="texon:606" /chromosome="19" /map="19943.3-q13.4"	<pre>AB join(37433840,39954050,44964655,65006759, 77147847,91789543) /product="kallikrein-like protein 5" join(37433840,39954050,44964655,65006759,</pre>
8 8 8 8 6	RESULT 8 AF135025 LOCUS DECINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE TITLE MEDLINE PUBMED REFERENCE AUTHORS TITLE AUTHORS TITLE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REMARK COMMENT FEATURES BOU	mRNA mRNA

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TLQCANISILEDKLCHWAYPGHISDSMLCAGLWGGGRGSCQGDSGGPLVCNGTLAGVV
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                                                                                                                                                                                            note="kallikrein 9; synonyms: KLK-L3, kallikrein-like
                                                                                                                                                                                                           9264. .9420,9586. .9715))
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complement(2594 ^~~~
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346. .6411
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3558. .3700
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4042. .4139
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8634. .8910
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family="MER33"
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11097. .11128
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>>05. .5712

/rpt_family="L3"

5878. .601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-007-2000) DOE Joint Genome Institute, Lawrence Livermore National Laboratory, Livermore, CA 94550 on Oct 12, 2000 this sequence version replaced gil-1458725.

Map and sequence oriented from centromere to q-telomere. BC349142 (CTC-518B2) overlaps BAC BC85745 (CTB-147C22, AC011483) on the left from bases I to 2,256 of this accession, and overlaps BAC BC892989 (CTD-3187F8, AC063977) on the right from bases 120,922 to 132,323 of this accession. Additional chromosome 19 map and sequence information are available at:

http://www.bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                 AC011473 132323 bp DNA linear PRI 12-OCT-2000 Homo sapiens chromosome 19, BAC BC349142 (CTC-518B2), complete
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ISPR"
                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lamerdin, J. B., McCrady, P. M., Skowronski, E., Viswanathan, V., Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Barkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Awila, J., Liu, S., Andreise, T., Trankheim, M., Attix, C., Andre, K., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Ow, D., Sequence, analysis of chromosome 19q13.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 132323)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(<77. .339,505. .664,1179. .1248))
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DOB Joint Genome Institute.
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                                                                                                                                                                                                                          sapiens (human)
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9534 AAGGAGGGC 9543
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                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                            sequence
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FSTFQCGGILVHRQWVLTAAHCISDNYQLWLGRHNLFDDBNTAQFYHYSBSFPHFGFN
MSLLENHTRQADEDYSHDLMLLRLTEPADTITDAVKVVELPTEEPEVGSTCLASGWGS
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COMPLEMENT ()OIN (<13552. .13704,14377. .14530,14678. .14917,
15416. .15569,19204. .>19246))
                                                                                                                                                                                                                                                                                                                                                                                                                   AF243527 230000 bp DNA linear PRI 21-NOV-2000
Homo sapiens serine protease gene cluster, complete sequence.
AF243527
                                                                  947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MWFLVLCLALSLGGTGAAPPIQSRIVGGWECEQHSQPWQAALYH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (28000) Gan, L., Lee, I. Smith, R., Argonza-Barrett, R., Lei, H., McCuaig, J., Moss, P., Paeper, B. and Wang, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 230000)
and L. Lee.I., Smith,R., Argonza-Barrett,R., Lei,H., McCuaig,J.,
Moss,P., Paeper,B. and Wang,K.
Direct Submission
Submitted (109-MRA-2000) Chiroscience R & D Inc., 1631 220th St. St
Bothell, WA 98021, USA
Location/Qualifiers
                                                                                    CCCCACCCTTAACTIGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCTCCATCAC
                                                                                                                                       TICCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCC
                                                                                                                                                               Moss, P., Paeper, B. and Wang, K. Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region
20510030
                                                            CCCCACCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="renal kallikrein"
complement (join(6963. .7118,7668. .7804,7923.
9482. .9641,11472. .11517))
/gene="KLKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join(<6963. 7118,7668. 9482. 9641.11472. >11517))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="serine protease"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (<6963. .>11517)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29482 GGGGTCTGTGGGGCCCTGTGGACATGGCATCCCTGGAGTCTACACCTATATTTGCAA 29423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _protein_id="AAG23256.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PBAYGS PCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLL
LLQGBQLRTRSVTHRVTHARARQSGPLIDERTDBHDLALLKLARAVVLGPRVRALQLPY
KAQQBQQCQVAGWTTAARRYKYKKGLTGSSITILSPRECEVPYPGVVTNNMICAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="kallikrein 10; synonyms: NES1, PRSSL1"
complement(join(14351. .15033,15498. .15631,15963. .16237,
17131. .17371,19124. .19220,19708. .19779))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name="gtSG30247"
/note="RH48452, WIAF-3662-STS"
/note family="MIR"
/rpt family="MIR"
complement(join(14881. .15033,15498. .15631,15963. .16237,
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7787. 1701.
                  complement(11133. .11411)
/rpt family="Alusg"
11412. .11515
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complement(11989. .12069)
/rpt_family="MIR"
complement(12070. .12390)
                                                                                                                                                                                                         complement(12391. .12498)
/rpt_family="MIR"
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complement(12694. .12976)
rpt_family="L2"
:2993. .13101
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17913. .17932
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13287. .13393
                                                                                                                                                                                                                                                .12606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="KLK10"
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1680.
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HLVSREEGERMYPGQITQNMLCAGDEKKGKDSCQGDSGGPLVCGDHLRGLVSWGNIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGL
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TSPRENPPTLANGASDVGKTFPQKKCEDAYPGQTTDGWYCAGSSKGADTCQGDSGGPLVC
COMPLEMENT (join (<190990. 191122,191573. 191709,
194324. 134589,197048. 197204,19770. >197412))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKLGLLCALLSLLAGHGWADTRAIGAEECRPNSQPWQAGLFHLT
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                                                                                                                            'codon_start=1
'produce="stratum corneum trypsin-like serine protease"
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'db_xref="GI:11244763"
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151186, .151433,155052, .155208,155948, .155987))
/note="serine protease; also called neurosin or zyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSWGDYPCARPNRFGVYTNLCKFTKWIQETIQANS"
complement(join(4146834. 146986,149628. 149764,
151186. 1.51433,155052. 155208,155948. .>155987))
/product="protease M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<165420, .165575,167672, .167808, 168124, ..168371,169651, .169798,170211, .>170283))
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complement(join(c183943. .184098.185635. .188768,
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187865. .188127,188293. .188452,188967. .189036)}
/note="serine protease; also called ovasin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="stratum corneum chymotryptic enzyme"
complement(join(165420. 165575,167672. 167808,
168124. 168371,169651. 169798,170211. 170283))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (<165420. .>170283)
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/protein_id="AAG33362.1"
/db_xref="GI:11244767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSKEKPGVYTNVCRYTNWIQKTIQAK"
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/protein_id="AAG33361.1"
/db_xref="GI:11244766"
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/product="protease M"
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                                                                      'gene="KLK5
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66074. .>66229)
/gene="KLK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .45955,46099. .46235,
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|oin(61139. .61184,62391. .62550,64142. .64428,64542. .64678,
                                                                                                                                                                                   / Godon start== processe // Godon start== processe // Godon start== processe // Product="AGO processes" // Product="AGO processes" // Protein id="AGO3354.1" // AGO354.1" // A
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CWGVLGGTTSWGPEPCALPERAVYTKVHYRKWIKOTIAANP"
COMPLement (joint <9460. . 94754,96027. .96163,96247. .96497,
96919. .97081,98345. .>98405)
Product="serine protease"
Complement (joint (94602. .94754,96027. .96163,96247. .96497,
96919. .97081,98345. .98405))
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EPEEFLTPKKLQCVDLHVISNDVCAQVHPQKVTKFMLCAGRWTGGKSTCSGDSGGPLV
CNGVLQGITSWGSEPCALPERPSLYTKVVHYRKWIKDTIVANP"
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RGRAVCGGYLVHPQWVLTAAHCIRNKSVILLGRHSLFHPEDTGQVFQVSHSFFHPLYD
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MSLLKHQSLRPDEDSSHDLMLIRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSI
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Qaalvmenelfcsgvlvhpqwvlsaahcronsytiglglhsleadqebcsgwyeasls
Vrhpennrpllandlwlikldssvsssdtirsisiasgcptagnsclvsgwgllangr
MPTVLQCVNVSVVSEBVCSKLYDPLYHPSMFCAGGGHDQKDSCNGDSGGPLICNGYLQ
                                                           .14530,14678. .14917,
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/product="stratum corneum trypsin-like serine protease"
complement(join(131301. .131456,136310. .136443,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<131301. .131456,136310. .136443, 136529. .136785,137525. .137690,140255. .>140303))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="prostate specific antigen"
20in(42595. .42640,43880. .44039,45669.
47614. .47769)
/gene="KLK3"
/product="ACO protease"
complement(join(13352, .13704,14377.
15416. .15569,19204. .19246))
/note="serine protease"
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/protein_id="AAG33355.1"
/db_xref="G1:11244760"
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/db_xref="GI:11244762"
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/gene="KLK3"
join(<42595. . 426</pre>
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/gene="KLK3"
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/gene="KLK2"
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Homo sapiens chromosome 19 clone RP11-10111, WORKING DRAFT
SEQUENCE, 32 unordered pieces.
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TLQCANISILENKLCHWAYPGHISDSMLCAGIWEGGRGSCQGDSGGPLVCNGTLAGVV
SGGAEPCSRPRRPAVYTSVCHYLDWIQEIMEN"
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Submitted (10-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9653152.
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Center code: WUGSC
                                                                                                                                                                         Indels
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Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
                                                                                                                   Query Match 33.9%; Score 370; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 3.6e-208;
Matches 370; Conservative 0; Mismatches 0;
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* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                        Consensus quality: bases at least 030
Consensus quality: bases at least 020
Consensus quality: bases at least 020
Insert size: 135000; agazose-fp
Insert size: 139234; sum-of-contigs
Quality coverage: 3.86 in 020 bases; agarose-fp
Quality coverage: 3.87 in 020 bases; sum-of-contigs
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	<pre>misc_feature 122124132649 /note="assembly_name:Contig57</pre>
	cloudend:1) vector ide:right" wisc_feature 132750142334 /note="assembly_name:Contig58"
	Query Match 22.8%; Score 249; DB 2; Length 142334; Best Local Similarity 99.7%; Pred. No. 5.3e-136; Matches 369; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
	OY 708 CCAGGGGGGATTCTGGGGGGCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCTG 767 DD 10984 CCAGGGTGATTCTGGGGGCCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGGTGTCTG 10925
	OY 768 GGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAA 827 Db 10924 GGGGTCTGTGGGGCCCTGTGGACAAGGCATCCCTGGAGTCTACACACTATATTGCAA 10865
	QY 828 GTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGACTG
,	OY 888 CCCAACCCTTAACTIGGGTACCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCAC 947 Db 10804 CCCCACCCTTAACTT-GGTACCCTCTGGCCTCAGAGCACCAATATCTCCTCCATCAC 10746
	OY 948 ITCCCTAGCTCCACTCTTGTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCC 1007 DD 10745 ITCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCC 10686
	OY 1008 CITCTAAGACCCACGAGGGGGGGGAGGGGGGGGAGTGTGCAATAGTCTGGAATAAATA
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RESULT 13 AC140096/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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/organism="pan troglodytes"
/mol.type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-63K10"
/clone=lib="RP43"
/lone="cone lib="RP43"
/note="cone overlaps with GenBank Accession Number AC137782 clone CH251-355A20 (center project name dhz)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /noce="assembly_fragment"
113257. .174724
/nocte="clone overlaps with GenBank Accession Number
47013339 - Conse CH251-126024 (center project name dxa)"
129209. .174724
                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be reserved.

* This gequence as soon as it is available and the accession number will be preserved.

* 47271 gap of unknown length

* 47371 S8115: contig of 10745 bp in length

* 58116 S815: gap of unknown length

* 61051 61050: contig of 1035 bp in length

* 61447 71536: contig of 6090 bp in length

* 65447 71536: contig of 6090 bp in length

* 83140 83139: contig of 11803 bp in length

* 83240 85133: gap of unknown length

* 83240 85133: gap of unknown length

* 83240 85133: gap of unknown length

* 83240 85133: gap of unknown length

* 83240 85133: gap of unknown length

* 83240 85133: gap of unknown length
                                                                                                                                                                                          Insert size: 150000; agarose-fp
Insert size: 173824; sum-of-contigs
Quality coverage: 15.91x in Q20 bases; agarose-fp
Quality coverage: 13.73x in Q20 bases; sum-of-contigs
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 172841 bases at least Q40 Consensus quality: 173490 bases at least Q20 Consensus quality: 173737 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 88837: Contig of 3604 bp in length
8 129108: Contig of 40171 bp in length
1 129208: gap of unknown length
9 1 174724: Contig of 45516 bp in length.
Location/Qualifiers
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/note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment
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HTGS PHASE2; HTGS DRAFT.
Pan trogolodytes
(chimpanzee)

Eukaryota; Metazoa; (chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

Lobaes 1 to 174724)
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Chu, G., Coleman, B., Coleman, H., Engle, J., Ho, S.-L., Hu, P.,
Hurle, B., Idol, J.R., Karlins, B., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paquirigan, C., Pearson, R., Portnoy, M.E., Sison, C., Stantripop, S., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D., Inchesis and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC140096 174724 bp DNA linear HTG 14-JUN-2003
Pan troglodytes clone RP43-63K10, WORKING DRAFT SEQUENCE, 10
ordered pieces.
                                                                                                                                                                                                                                          211 AACTCACAGCGGTGGCAGGTGGGGGCTGTTTGAGGGCACCAGCCTGCGCTGCGGGGGTGTC 270
                                                                                                                                                                                                 211 AACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCACCAGCCTGCGCTGCGGGGGGTGTC 270
91 TTTTCCCCCAGACTTTGGAAGTGACCCACCATGGGGCTCAGCATCTTTTTGCTCCTGTGT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-FEB-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 174724)
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Submitted (14-UDN-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 14, 2003 this sequence version replaced gi:29725783.
                                                                 151 GITCITGGGCTCAGCCAGGCACCACCGAAGAITTTCAAIGGCACTGAGIGTGGGCGI
                                                                                                                               151 GTTCTTGGGCTCAGGCAGCCACCGAAGATTTTCAATGGCACTGAGTGTGGGGCGT
                                                                                                                                                                                                                                                                                                                                271 CTTATTGACCACAGGTGGTCCTCACAGGGGCTCACTGCAGGGGCAG 317
                                                                                                                                                                                                                                                                                                                                                                   271 CTIAITIGACCACAGGTGGGTCCTCACAGGGGGCTCACTGCAGGGGGCAG 317
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Green, E.

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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On Nov 22, 2002 this sequence version replaced gi:22218452
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/clone_lib="CH251"
                                                                                                                                                                                        Center clone name: 355A20
                                                                                                                                                               Center project name: dhz
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159979: gap of
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174798: gap of
                           -- Genome Center
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  COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38045 CCCCACCCCTTAGCTTGGGTACCACTCTGGCCCCCAGAGCACCAATATCTCCTCCATCAC 37986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1008 CITCIAAGACCCACGAGCGGGGTGAGAAGTGTGCAATAGTCTGGAATAATATAATG 1067
                                                                                                                                                                  0;
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Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 948 TICCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 200792)
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Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                         828 GTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCAC
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                                                                                                                                                                                                                                                                                                              768 GGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAA
                                                                                                                                                                    Gaps
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0
                                                                                                                     Length 174724;
                                                                                                                                                               3; Indels
                                                                                                                     19.9%; Score 217; DB 2; I 99.2%; Pred. No. 6.5e-117; tive 0; Mismatches 3;
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clone_end:SP6
vector_side:right"
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                                                                                                                                                                    Matches 367; Conservative
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                                                                                                                                                 Best Local Similarity
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DEFINITION
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TITLE
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* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 28307 28406: gap of unknown length

* 28407 37856: contig of 2850 bp in length

* 37857 73522: contig of 3856 bp in length

* 73623 83677: contig of 3856 bp in length

* 73623 83677: contig of 9450 bp in length

* 83568 836677: contig of 9450 bp in length

* 83688 838677: contig of 9450 bp in length

* 83688 838677: contig of 9450 bp in length

* 83688 888177: contig of 9450 bp in length

* 83688 888177: contig of 9450 bp in length

* 88918 125611: contig of 5150 bp in length

* 88918 125611: contig of 3694 bp in length
                                                                                                                                                                                                                                                                                                                      The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contrig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by FCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 196656 bases at least Q40 consensus quality: 197883 bases at least Q40 consensus quality: 197883 bases at least Q20 lnsert size: 215000; agarose-fp lnsert size: 215000; agarose-fp plast coverage: 9.03x in Q20 bases; sum-of-contigs Quality coverage: 9.73x in Q20 bases; sum-of-contigs
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186482: gap of unknown length
193344: contig of 6862 bp in length
193444: gap of unknown length
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Center: NIH Intramural Sequencing Center
Center code: NISC
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                                                                                        Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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Direct Submission
Submitted (10-JUN-2000) Genome Sequencing Center, Washington
Submitted (10-JUN-2000) of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9653152.
Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 3.86 in Q20 bases, agarose-fp
Quality coverage: 3.87 in Q20 bases; sum-of-contigs
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gap of unknown length
contig of 1185 bp in length
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gap of unknown l
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gap of unknown l
contig of 2961 b
gap of unknown l
contig of 2861 b
gap of unknown l
contig of 2861 b
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contig of 3209 b
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                                                                                    The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 142334) Waterston, R.H.
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1 (bases 1 to 142334)
Waterston, R.H.
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Homo sapiens chromosome 19 clone RP11-10111, WORKING DRAFT
SEQUENCE, 32 unordered pieces.
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clone_end:SP6
vector_side:left"
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AC073185.4 GI:9838034
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
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36: gap of unknown length
121: gap of unknown length
157: contig of 4636 bp in length
157: contig of 6159 bp in length
7516: gap of unknown length
7516: gap of unknown length
7510: contig of 6159 bp in length
7510: contig of 4194 bp in length
66249: gap of unknown length
66349: gap of unknown length
77980: contig of 633 bp in length
77980: contig of 633 bp in length
77454: contig of 6764 bp in length
77454: contig of 6764 bp in length
84318: gap of unknown length
84318: gap of unknown length
84318: gap of unknown length
84318: gap of unknown length
84418: gap of unknown length
84418: gap of unknown length
84419: contig of 5670 bp in length
84419: contig of 5670 bp in length
94419: contig of 5670 bp in length
94519: gap of unknown length
100165: gap of unknown length
100165: contig of 7659 bp in length
115093: contig of 7659 bp in length
122022: contig of 7659 bp in length
12411513: gap of unknown length
12412123: gap of unknown length
12503: contig of 9585 bp in length
12650: 132749: gap of unknown length
12750: 142334: contig of 9585 bp in length
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3965 ACCCATTCCCGGAICTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCC 4024
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11.6%; Score 127; DB 2; Length 142334;
Best Local Similarity 100.0%; Pred. No. 3.1e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0;
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Search completed: June 20, 2004, 07:34:57 Job time: 4629 secs

Human Human Human

Aaa95944 Aaf65654

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Run on:

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AAA77671;
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Aaa27075 Human PRO
Aaa27075 Human PRO
Aa68378 Novel hum
Ac04480 Human cDN
Acd68024 Novel hum
Ac18062 Human cDN
Add70708 Human cDN
Add3998 Human cDN
Add38152 Human cDN
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                                                                                                               June 20, 2004, 04:42:21; Search time 509 Seconds (without alignments) 9105.666 Million cell updates/sec
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Ade54341
Ade68024 M
Acd68024 M
Add18062 Add190708 H
Add393108 Add393108 Add393108 Add393108 Add393108 Add393108 Add393108 Add5005 Add5005 Add5005 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 Add5006 A
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
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Ade50732 F
Ade20344 F
Ade50255 F
Ade21813 F
                                                                                                                                                                                                                                                   Add39080
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                                          ABN45198
ABZ64830
AAF55401
AAF55198
ACH64659
ACH64659
ACH64659
ADD40034
ADD40034
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98US-0112850P.
99US-011554P.
99US-0123957P.
99US-0131445P.
99WS-0131445P.
99WS-0141037P.
99US-0141037P.
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99WO-US020594.
99WO-US020944.
99WO-US021090.
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(GETH ) GENENTECH INC.
WO200032221-A2
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12-JAN-1999;
12-JAN-1999;
12-MAR-1999;
28-APR-1999;
28-JUN-1999;
20-JUN-1999;
26-JUN-1999;
26-JUL-1999;
13-SEP-1999;
13-SEP-1999;
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Hillan KJ; Kuo SS, Paoni NF;

Gerber H, Klein RD,

Ferrara N, Gurney AL,

Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ,

nov kal

Human Human Human

ABK94900 AAL59914 ADE21564 AAH98653

ABK30369

ADD40262 ADE50483 ADE20095 ADE50006

ADD38831

Result No.

720 780 780 900 900 960

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ACTOTTGTTGGCCTGGGAACTTCTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA 1020
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TGCCTCAACCTCTCCATGGTCTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATC
                                                       Aceaecaacarearererecaeecesecereceeecaeearecereceaeereceaeererer
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                                                                                                                                                            CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG
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99US-0162506P.
99WO-US028313.
99WO-US028634.
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                                                                                                                                                                                                                    useful for preventing, diagnosting and treating diagnosing a cardiovascular, enouthellal or angiogeneis diagnosing a cardiovascular, endothelial or angiogeneis diagnosing a mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagnomists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA7721 and AAB24188 to AAB24415 represent
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                                                                             MUCLEIC ACIDS ENCODING PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
                                                                                                                                                                                                      The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCACTGCAGCGGCAGGTACTGGGTGCGCCTGGGGGAACACACCAGCCTCAGCCAC
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         Wood WI;
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Pred. No. 0;
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         Williams PM,
                                                                                                                                                                         61; Fig 81; 315pp; English
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Best Local Similarity 100.0%;
Matches 1091; Conservative 0
                                              2000-412154/35
           Watanabe
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Human, PRO polypeptide, membrane bound protein, receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
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                          GOGGCCCCCTGGTGTGTGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGG
                                                                                    CCCTGTGGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGGACTGG
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98US-0099741P.
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                         The present invention describes an antibody that binds to a human protein

(1) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;

PRO1927; PRO3567; PRO1925; PRO1293; PRO1303; PRO4344; PRO43454; PRO43407;

PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (1) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells.

Increased expression of genes encoding (1) can also be detected to diagnose tumours. Agents which inhibit the activity of (1), especially the antibodies, or an antisense oligonuclectide which hybridises to genes encoding (1), can be used to inhibit the present invention can be used to inducing cell death. Methods from the present invention can be used to inducing cell death. Methods from the present invention can be used in examples from the present invention for human PRO sequences. AACS8103 to AACS812 and AAR24021 to AAAS812 and AAR24021 to AAAS812 and AAR24021 to Prepresent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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   50; Fig 23; 226pp; English.
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Matches 1091; Conservative
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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY9340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences modding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR polypeptides from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.
                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI;
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98US-0106384P.
98US-0106464P.
98US-0106902P.
98US-0106912P.
98US-0106913P.
98US-0106913P.
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P-PSDB; AAY99393
29-OCT-1998;
29-OCT-1998;
30-OCT-1998;
30-OCT-1998;
30-OCT-1998;
30-OCT-1998;
30-OCT-1998;
30-OCT-1998;
30-OCT-1998;
10-NOV-1998;
17-NOV-1998;
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18-NOV-1998;
18-NOV-1998;
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1 CAAGCAGGICAICCCCTIGGIGACCTICAAAGAAGCAGAGAGAGAGAGAGAGGIGGGGGC 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
                                                                                                                                                                                                                                                                                                                                                                                                                               Fong S;
Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nuclacids may also be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe
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                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 107; 787pp; English.
                                                                                                                                                           23-JUN-1999; 99US-0141037P.
20-JUL-1999; 99US-0144758P.
01-SEP-1999; 99WS-014569BP.
01-SEP-1999; 99WO-US020111.
29-OCT-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028313.
16-DEC-1999; 99WO-US028313.
16-DEC-1999; 99WO-US020851.
16-DEC-1999; 99WO-US020851.
16-DEC-1999; 99WO-US020851.
                                                                                                                            2000WO-US004342.
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                                              WO200078961-A1
          Unidentified,
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                                    ACCAGCAGCGTTCAACCCTTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGC
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Hillan KJ;
Watanabe Cl
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100.0%; Score 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches
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2000WO-US006884.
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P-PSDB; ABO33635.
11-FEB-2000; 24-FEB-2000; 24-FEB-2000; 22-MAR-2000; 215-MAY-2000; 217-MAY-2000; 23-MU-2000; 24-AUG-2000; 24-AUG-2000; 24-AUG-2000; 24-AUG-2000; 201-DEC-2000; 201-MEB-2001; 201-MIN-2001;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP,
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481 ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC 540

	H PR	01-SEP-1998;	98US-0098723P.	
541 CACGICTCAGGCTGGGGCATCACCACCACGGAACCCATTCCGGGAICTGCTCCAG 600	PR	01-SEP-1998; 02-SEP-1998;	98US-0098/49F. 98US-0098750P.	
541 CACGICICAGGCTGGGGCAICACCAACCACCACGGAACCCAIICCGGGAICTGCICCAG 600	PR	02-SEP-1998; 02-SEP-1998;	98US-0098821P. 98US-0098821P.	
601 TGCCTCAACCTCTCCATCGTCTCCCAATGCCACCTGCCATGGTGTATCCCGGGAGAATC 660	묎	09-SEP-1998;	98US-0099536P.	
	P. P.	09-SEP-1998;	98US-0099596P. 98US-0099598P.	
1	PR	09-SEP-1998; 09-SEP-1998;	98US-0099602P. 98US-0099642P	
	PR 90	10-SEP-1998;	98US-0099741P.	
i algastaatatggtgtgtgtgcaggcggcgtcccggggcaggatgcctgcc	R	10-SEP-1998;	98US-0099754P. 98US-0099763P.	
721 GGGGGCCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGG 780	PR PR	10-SEP-1998; 10-SEP-1998;	98US-0099792P.	
721 GGGGCCCCCGGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGGG 780	PR	10-SEP-1998;	98US-0099812P.	
	7 G	10-SEP-1998;	98US-0099815P. 98US-0099816P.	
TO CONTROLL OF THE PROPERTY OF	PR PR	15-SEP-1998; 15-SEP-1998;	98US-0100385P.	
	PR PR	15-SEP-1998;	98US-0100390P.	
	E E	16-SEP-1998;	98US-0100584F.	
	አ ፕ	16-SEP-1998; 16-SEP-1998;	98US-0100661P. 98US-0100662P.	
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–ფ	PR R	17-SEP-1998;	98US-0100684P.	
_	. H.	17-SEP-1998;	98US-0100711P.	
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	ያ ያ	18-SEP-1998;	98US-0100848P.	
CGAGCGGGTGAGAA	4 H	18-SEP-1998;	98US-0100849P. 98US-0101014P.	
1021 CGAGCGGGTGAGAGTGTGCAATAGTCTGGAATAAATATAAATGAAGGAGGGGCAAA 1080	ж ж	18-SEP-1998; 18-SEP-1998;	98US-0101068P. 98US-0101071P	
1081 ABABABABABA 1091	됐	22-SEP-1998;	98US-0101279P.	
1081 AAAAAAAAA 1091	. H.	23-SEP-1998;	98US-0101472P.	
	7. Y.	23-SEP-1998; 23-SEP-1998;	98US-0101474P. 98US-0101475P	
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104480 standard; cDNA; 1091 BP.	PR	23-SEP-1998;	98US-0101479P.	
104480;	ጟጟ	24-SEP-1998; 24-SEP-1998;	98US-0101738P. 98US-0101741P.	
OCT-2003 (first entry)	RR	24-SEP-1998;	98US-0101743P. 98US-0101915P.	
an cDNA encoding secreted/transmembrane protain pp01202	A A	24-SEP-1998; 29-SEP-1998;	98US-0101916P. 98US-0102207P.	
an: ss: gene, convered mountain the second s	PR PR	29-SEP-1998; 29-SEP-1998;	98US-0102240P.	
diant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer:	# E	29-SEP-1998;	98US-0102330P.	
.undl cortical capillary; endothelial cell growth; wound healing; .mulated T-lymphocyte proliferation; immune response suppression	PR S	30-SEP-1998;	98US-0102331P. 98US-0102484P.	
matal heart hypertrophy; cardiac insufficiency disorder;	¥ ¥	30-SEP-1998; 30-SEP-1998;	98US-0102487P. 98US-0102570P	
inophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;	PR ፍር	30-SEP-1998;	98US-0102571P.	
tion;	. W. C	01-0CT-1998;	98US-0102687P.	
o sapiens.	r r	06-0CT-1998;	98US-0102965P. 98US-0103258P.	
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,	oyers PJ, Mith		GTGACCTTCA	TGAGATTCCC TGAGATTCCC	TGCTCCTGTGT TGCTCCTGTGT	agtgregecer
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      ACTITIGITGGCCTGGGAACTTTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA 1020
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                                                               Human; secreted and transmembrane protein; PRO; gene therapy; vaccine; tissue typing; chromosome identification; vaccine; gene; ss.
GGGGGCCCCCTGGTGTGGGGGAGTCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGG
                                                                                     CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG
                                                                                              ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCCTTAA
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                                                                                             Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.
                              Fong S;
Hillan KJ;
Watanabe CJ
                                                                                                                                                                                                                                                                                   181 AAGATTTTCAATGGCACTGAGTGTGGGGGGTAACTCACAGCCGTGGCAGGTGGGGGGCTGTTT
                                                                                                                                                                                                                                                                                                                                                                   GACTGGACCGAGAGGACACAGGGGCTTCTCTGTGAGCCATCCGGGCTACCTGGGA
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                        Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;
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100.0%; Score 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches
                                                                                                                                Claim 2; Fig 107; 561pp; English.
        (GETH ) GENENTECH INC.
                                                                   WPI; 2003-585292/55.
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CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG
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                                                                                                                                                          Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;
gene mapping; genetic disorder.
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ADC18062
ID ADC18062 standard; cDNA; 1091 BP.
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The invention relates to human PRO polypeptides and the polynucleotides encoding them. The sequences are useful in the preparation of a medicament for treating a condition responsive to a PRO polypeptide. The polypeptides are useful in a number of functional biological assays, as molecular weight markers for protein electrophoresis and as therapeutic
    Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.
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          Human; ss; gene; secreted protein; transmembrane protein, PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthitis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTTCCCCTAGCTCC
                                                                               ACTOTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA
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                                                                                                      Actitiditideccridedaacriciideaacriraacriciideccrirciaadaccca
                                                                                                                                           Human cDNA encoding secreted/transmembrane protein PRO1303
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Ferrara N, Gurney AL, B Desnoyers L, Eaton DL, Fe owski PJ, Grimaldi JC, Gur WA, Smith V, Stewart TA, Botstein D, Desno Paoni NF, Roy MA, ns PM, Wood WI; (GETH) GENENTECH INC Baker KP, Botstein Gao W, Goddard A, Pan J, Paoni NF, 1

Fong S; Hillan KJ; Watanabe CK;

WPI; 2003-874602/81 P-PSDB; ADD70709.

Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle cells and are useful for treating diabetes or hyper- or hypo-insulinemia.

ô 961 ACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA 1020 120 120 180 180 240 300 300 360 360 420 420 480 480 540 540 600 099 009 99 720 720 780 840 780 840 900 900 960 9 9 ACAGGGAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTTGGAAGTGACCACC ATGGGGCTCAGCATTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACCCCC GAGGGCACCAGCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCG GAGGGCACCAGCTGCGCTGCGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGG GCTCACTGCAGCAGCAGCAGCAGCTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCTCG GACTGGACCGAGCAGATCCGGCACACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA GCCTGGAGGCACGAGGACGACGACGACGGCTGCTGCTGCGGCTGCGCCTGCCCGGCTGCGCGTA ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACGCTGGCACCGAGGGGCGT CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTTCCATTCCCCTAGCTCC CAAGCAGGICAICCCTIGGIGACCTICAAAGAGAAGCAGAGAGGGCAGAGGGGGGG ATGGGGCTCAGCATCTTTTTGCTCCTGTGTTCTTGGGCTCAGCCAGGCAGCCACCAC AAGATTTTCAATGGCACTGAGTGTGGGGCGTAACTCACAGGCGGTGGGAGGTGGGGGCTGTTT AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTT GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA GCCTCGACGAGCCACGACCACGACCTCCGGCTGCGGGCTGCGCCTGCCGTCCGGCGTA ACCAGCAGCATCAACCCCTGCCCCAATGACTGTGCAACCGCTGGCACCGAGTGC CACGTCTCAGGCTGGGGCATCACCAACCACGGAACCCATTCCCGGATCTGCTCCAG CACGTCTCAGGCTGGGGCATCACCAACCACGGAACCCATTCCCGGATCTGCTCCAG TGCCTCAACCTCTCCATCGTCTCCCATGCCATGGTGTGTATCCCCGGGAGAATC GGGGGCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGGG CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG CCCTGTGGGACAGATGGCATCCCTGGAGTCTACACCTATATTTGGAAGTATGTGGACTGG ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCTTAA Gaps 0; The invention relates to an isolated PRO polypeptide (secreted Length 1091; Indels 9; ., DB Query Match 100.0%; Score 1091; Best Local Similarity 100.0%; Pred. No. 0; Matches 1091; Conservative 0; Mismatches English SEQ ID NO 193; 553pp; 2, 61 19 121 121 181 181 241 301 301 361 361 421 421 481 481 541 721 841 841 541 601 601 199 661 781 721 781 901 Claim SXXS g à d ŏ g ð 임 g ò g δ qq ð 임 δ Op à ð g ŏ 엄 ò d à g à q qq 셤 ð à à

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, Fong S;
Hillan KJ;
, Watanabe CK;
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                       r, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, F
Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D.
                                                                                                                                                 Human cDNA encoding secreted/transmembrane protein PRO1303.
                                                                                                     ADD39785 standard; cDNA; 1091 BP
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99WO-US028313
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22-MAY-2000;
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08-NOV-2000;
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28-FBB-2001;
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Pan J, Paoni
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The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequences as to a maino acid sequence chosen from 123 fully defined sequences as or amino acid sequences enclosen from 123 fully defined sequences as or without their associated signal peptides. Also include are the nucleotide (Ma) sequences encoding PRO, a vector comprising the PRO NA, a comprising PRO fused to a heterologous amino acid sequence, and an anti-encomprising the vector, producing PRO, a chimaeric molecule PRO antibody. Pro is useful as molecular weight markers for protein useful for tissue typing. PRO and PRO NA are useful as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is useful for tissue typing. PRO and PRO NA are useful in development and screening useful reagents. PRO NA is also useful in development and screening useful reagents. PRO NA is also useful in development and screening useful reagents. PRO 1410 propeptides are useful for suppressing immune response. PRO1246 and PRO1410 polypeptide is useful for reacting cancerous tumours. PRO1250, PRO1418 and PRO146 polypeptide is useful for treating cardiac insufficiency disorders. PRO1546 polypeptide is useful for treating cardiac insufficiency disorders. PRO1546 polypeptide are useful for treating tumours. PRO1246 and PRO1450 polypeptides are useful for treating bence and obesity. PRO1255, PRO1418 on PRO1418 and wound healing. PRO1156, PRO1555 and PRO1418 and wound healing. PRO1255 and PRO148 are useful for treating berger disease or other nephropathies associated with Schonlein-fleaten purpura, coellac disease, dermattitis, herpetiformis or Crohn's Glassase. PRO1478, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1419, PRO1265, PRO1410 and PRO1575 are useful in treating thalassaemias. The present condess a PRO protein of the in
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New secreted and transmembrane PRO polypeptides useful for treating cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper-hypo-insulinemia, sports injuries and arthritis.
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                                 ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGGCTGGCACCGAGTGC
                                                                           TGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTATCCCGGGAGAATC
                                                                                                                                                                                                GCCTCGACGAGCACGACCACGGCTGCTGCGGCTGCGCCTGCCCTGCCCGTCCGCGTA
                                                                                                          CACGICICAGGCIGGGGCAICACCAACCACGGAACCCAITCCCGGAICIGCICAG
                                                                                                                               TGCCTCAACCTCTCCATCGTCTCCCATGCCATGCCATGGTGTGTATCCCGGGAGAATC
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Homo sapiens

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RESULT 11

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481 ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC
                                                     GGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGG
                                                                                                                                                                                                                                                                     GGGGCCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGG
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                                  CACGICICAGGCIGGGGCAICACCAACCACGGAACCCAITCCCGGAICIGCICCAG
                                                                                                  TGCCTCAACCTCTCCATGCTCTCCCATGCCATGCTGTGTATCCCGGGAGAATC
                                                                                                                                                                    ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCACCCTTAA
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Gurney AL, Hillan KJ;
A, Tumas D, Watanabe (
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                                                                                                                                                                                                                                          Novel isolated PRO polypeptide, useful for treating cancerous tumors, cardiac insufficiency disorders, wound healing, diabetes mellitus, thalassemias.
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Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gu:
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA,
Williams PM, Wood WI;
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28-FEB-2001; 2001WO-US006520.
01-WAR-2001; 2001WO-US006666.
01-UJN-2001; 2001WO-US017800.
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29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
04-SEP-2001; 2001WS-US021735.
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                                                                                                                                                                                                                                                                                                                      ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCACCCCCACCCCTTAA
TGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATC
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540 , Fong S; Hillan KJ; , Watanabe CK; ô 420 480 540 009 099 099 720 780 300 300 360 360 420 480 009 720 120 180 240 240 120 180 9 09 GCCTCGACGAGCCACGAGCACGACCTCCGGCTGCTGCGCCTGCCCCTGCCCCTCCGCCTA GGGGGCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCCTGGGGGTCTGTGGGG 61 ACAGGGAAAGGGTGACCTCTGAGATTCCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC 61 ACAGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCCAGACTTTGGAAGTGACCACA 121 AIGGGGCICAGCAICITITIGCICCIGIGIGIGITCITIGGGCICAGCCAGGCACCACGCACCG GAGGGCACCAGCCTGCGCGCGCGGGTGTCCTTATTGACCACACGGTGGGTCCTCACAGCG 241 GAGGGCACCAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGG GACTGGACCGAGCAGATCCGGCCACAGCGGCTTCTCTGTGACCCCATCCCGGCTACCTGGGA GACTGGACCGAGCAGATCCGGCACCAGCGCTTCTCTGTGACCCATCCCGGCTACCTGGGA GCCTCGACGAGCACGACCACGACCTCCGGCTGCGGCTGCGCCCTGCCCCTCCGCGTA ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC Accadotacetricaacecerdecetracecardacrereraceacecerdecaced CACGICICAGGCIGGGGCATCACCACCACCACGGAACCCAITCCCGGAICTGCICCAG CACGICTCAGGCTGGGGGCATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCAG TGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATC TGCCTCBACCTCTCCATGGTCTCTCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATC caagcaggrearcerregreacerreaagagaagagagagagagagagagagagggggg 181 AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCGGTGGCAGGTGGGGGCTGTTT Gaps Novel isolated PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor. or . 0 The invention relates to an isolated PRO polypeptide (secreted Ferrara N, Gurney AL, H 'A, Tumas D, Indels Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gur Pan J, Baoni NF, Roy MA, Smith V, Stewart TA, Williams PM, Wood WI; L, Eaton DL, Grimaldi JC, G 9. .. DB Query Match
100.0%; Score 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches Claim 2; SEQ ID NO 193; 550pp; English. Desnoyers Botstein D, Desno (GETH) GENENTECH INC. WPI; 2003-786999/74. P-PSDB; ADD39309. ч ч 361 481 481 541 541 601 661 661 721 241 301 361 421 421 601 g g 셤 $\dot{\circ}$ g g ga g 원 8 8 $\dot{\delta}$ g ò qq ð ð 8 g à à à à δ à

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GGGGGCCCCCTGGTGTGGGGGAGTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGG 780
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                                CCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG
                                                                ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCCTTAA
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                                                      CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTTCCCCTAGCTCC
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                                         New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773, PRO1244, PRO1246, useful for treating cancerous tumors, cardiac insufficiency disorders, wound healing, Crohn's disease, celiac disease
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100.0%; Score 1091; DB 9; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0;
                                                                                                  Claim 2; SEQ ID NO 193; 555pp; English
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    WPI; 2003-765477/
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Watanabe CK;
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    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diseles; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
                                                                                               961 ACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA
                                                                                                                                                 1021 CGAGCGGGGTGAGAGAGAGAGAGATGCTGGAATAAATATAAATGAAGAGGGGCGAAA
 841 ATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTCCACCTCCACCCCCACCCCTTAA
                                                                                                                                   CGAGCGGGGGGAGAGGGGCAATAGTCTGGAATAAATATAAATGAAGGGGGCAAA
                             CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTTCCCCTAGCTCC
                                                   901 CTTGGGTACCCCTCTGGCCCTCAGAGCACCAATATCTCCTCCATCACTTCCCCTAGCTCC
                                                                                961 ACTCTTGTTGGCCTGGGAACTTCTTGGAACTTTAACTCCTGCCAGCCCTTCTAAGACCCA
                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding secreted/transmembrane protein PRO1303.
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             or
            The invention relates to an isolated PRO polypeptide (secreted
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100.0%; Score 1091;
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PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
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Hillan KJ;
Watanabe C
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Gurney AL, F
A, Tumas D,
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Grimaldi JC, Gu
V, Stewart TA,
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98US-0106919P

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Paoni NF, Ro
s PM, Wood WJ
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P-PSDB; ADD40263.
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06-JAN-2000; 2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BX110362 BX110362	AI394679 tg24b03.x	BC035385 Homo sapi	BG230967 nag78a04.
SUMMARIES	TD	BX110362	AI394679	1186 11 BC035385	BG230967
	BB :	13	σ	11	12
% Query	Length	472	469	1186	264
% Query	- 1	29.8	23.3	22.9	19.8
	Score	325	254	250	216
Result	No. S	н	ر 2	æ	4

4072	2115	2909	BQ270082 ik33g02.y	7000	2408	329	3356	1474	1852	12883 tigr-gss	16427 AUF 105	602	CH240 46	Mus mus	BY70902		Tetraod	UI-R-I	wn73£06	BF353225 QV3-HT063	tigr-	EBed01	BF073014 219560 MA	376109	1668	1 zt26g09	19 UI-H-B	179 K-ESTO	073		7 QV2	RC3-BN00	AMGNINUC:	Ö	26	16451	7 zt54a12.	93 K-ESTO		
AI554072 BX103516	S	σ	3 BQ270082	BT794700	œ	CA313295	9	BX514743	S	CE842883	CD646427	BG762809	CC558299	AK009217	BY709025	BX689949	CNSOSFCE	BI278918	AI924035	BF35325	CE737502	BM368334			CB776687		AW136489	047	37	339	AW820357	105	5	16	56	B716	29302		CHARLE TAKE	ALIGNMENTS
9	12	13	13	15	9	14	δ	13	σ	29	14	12	59	11	13	13	29	12	σ	10	S)	C)	0	\sim	~ #		0	12	10	14	10	10	14	14	12	14		15		
383 478	550	577	009	200	449	451	206	520	545	627	763	765	768	890	838	904	1002	149	224	242	255	287	351	389	394	400	402	405	457	464	482	483	491	498	512	515	517	523		
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Source

FEATURES

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Likix at:

www-bio.llnl.gov/bbrp/image.html

Insert Length: 1051 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bcu35385 1186 bp mRNA linear HTC 04-MAR-2003
Homo sapiens, Similar to kallikrein 12, clone IMAGE:4825490, mRNA.
BC035385
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 GGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.3%; Score 254; DB 9; Length 469; 100.0%; Pred. No. 2.5e-62; tive 0; Mismatches 0; Indels
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   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="IMAGE:2109677"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         814 ACCTATATTTGCAA 827
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BC035385
LOCUS
   AUTHORS
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ARNA linear EST 30-MAR-1999
tg24b03.x1 NCI CGAP CLL1 Home sapiens GDNA clone INAGE:2109677 3'
similar to SW:TRY3 CHICK 090629 TRYPSINOGEN 2-P29 PRECURSOR.
CONCains TAR1.b1 TAR1 repetitive element ;, mRNA sequence.
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                                              www.rrpd.de
www.rrpd.de
This clone is available royalty-free from RZPD;
contact RZDD (clone@rzpd.de) for further information. Seg primer:
Ml3r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AGACTTTGGAAGTGACCCACCATGGGGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACTITIGGAAGTGACCCACCATGGGCTCCAGCATCTTTTTGCTCCTGTGTGTTTTTGGG
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Pred. No. 2e-82;
0; Mismatches 1; Indels
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|mol_type="mRNA"
|db_xref="taxon:9606"
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Tel: +49 30 32639 101
Fax: +49 30 32639 111
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Query Match Best Local Si Matches 375;

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EST.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

A1394679/c LOCUS

DEFINITION

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AUTHORS TITLE JOURNAL

REMARK COMMENT

REFERENCE

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.,
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@aimage llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 257.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone=InAGE:422367"
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/note="vector: pAMPIO; cDNA made by oligo-dT priming.
/note="vector: pAMPIO; cDNA made by oligo-dT priming.
/note="vector: pAMPIO; cDNA made by oligo-dT priming."
/note="vector: pampio; cDNA made by oligo-dT priming. Protectionally cloned into the UDG sites of pAMPIO.
Size-selected on agarose gel, average insert size 500 bp. Primary inbrary; non-amplified. cDNA Library.
Preparation: David B. Krizman, Ph. D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
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183 bp mRNA linear EST 13-APR-1999

te49g02.xl Soares NFL T GBC S1 Homo sapiens cDNA clone

IMAGE:2090066 3' similar to TR:Q99920 Q99920 NES1=NORMAL EPITHELIAL

CELL SPECIFIC GENE 1. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACTICITGGAACTITAACTCCTGCCAGCCCTICTAAGACCCACGAGGGGGTGAGAGA 1036
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                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primatees; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 254)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Cancer Institute / National Institute of Dental Research Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Homo sapiens
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                                                                                                                                                                                                                                                     NULH MGC Project URL: http://mgc.nci.nih.gov
CONtact: MGC help desk
Email: ogapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkcvits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 71 Row: m Column: 9
This clone has the following problem: retained intron.
                                                                                                                    Mammalian
                                                                                                                                                    Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               802 ACCCATICCCGGATCTGCTCCAGTGCCTCAACCTCTCCATGCTCTCCCATGCCACCTGCC
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                                Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health,
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/mol type="mRNA"
/mol type="mRNA"
/clone="Laxon:9606"
/clone="Testis"
/clone_lib="MIH MGC 97"
/lab host="DHIOB"
/note="Dector: pBluescript"
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(bases 1 to 1186)
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/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHil9W, testis NHT, and B-cell NCI CGAP GCBl) were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302086, 682632-687239, 726408-728711, and 723096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
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Unpublished (2003)
Contact: Ina Rolfs
                                                                Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Inis clone is available royalty-free through LiNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 575 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 373.

1. .383
1 (bases 1 to 383)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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RZPDLIB; I.M.A.G.E. CDNA Clone Collection;

Ruman Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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BX103516 SOares NFL T GBC S1 Homo sapiens cDNA clone
IMAGD9980035152 ; IMAGE:2090066, mRNA sequence.
BX103516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 383;
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Pred, No. 5.9e-19;
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100.0%; Pred. No. ...
0; Mismatches
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Homo sapiens
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BX103516/c
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                        AUTHORS
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602693314F1 NIH_MGC_97 Homo sapiens CDNA clone INAGE:4825490 5',
MRNA sequence.
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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tobh Jibrary Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Close distribution: MGC close distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10738 row: 1 column: 03
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
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/organism="Homo sapiens"

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Homo sapiens
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                                                                                                                 /note="Organ: Testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHi; Site 2: Sall-XhoI gBluescript KS+); Site 1: BamHi; Site 2: Sall-XhoI gCtGggg); Oligo-dI primed using primer 5: -TTTTTTTTTTTTTTTTVN-3; size-selected for average insert size 2: Xb and normalized to ROT 5. This is primary library enriched for full-length clones and constructed using the Cap-trapper method (Carningi, in preparation). Library constructed by M. Brownstein (NIMM/WRRI, National Institutes of Health). Note: this is a NIMM/WGL Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 577)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Melton Amplified Mouse E16 5 Pancreas 3 M16S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQ129094 1127h02.x1 Melton Amplified Mouse El6 5 Pancreas 3 Mf6S1 A Mus musculus cDNA clone IMAGE:5943026 3' similar to TR:Q9Z1H1 Q9Z1H1 Q9Z1H1 PG5 GENE, 3' END ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvill, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center This clone is available royalty-free through LLNL; please contact the IMAGE consortium (info@image.llnl.gov) for further information Seq primer: -40UP from Gibco High quality sequence stop: 235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAGTGACCCACCATGGGGGTTCAGCATCTTTTTGCTCCTGTGTGTTCTTGG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 GGAAGTGACCCACCATGGGGCTCAGCATCTTTTTGCTCCTGTGTTCTTTGG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%; Score 52; DB 12; Length 550;
100.0%; Pred. No. 3.4e-05;
tive 0; Mismatches 0; Indels
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/lab_host="DH108"
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                                                                                                 /clone lib="NIH MGC 97"
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                                            /clone="IMAGE:4825490"
/lab host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:5943026"
                     db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrine Pancreas Consortium Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ129094.1 GI:20203005
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Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ129094
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KEYWORDS
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/clone="IVAGGE:5782850"
/tissue_type="Purified pancreatic islet"
/lab.hoft="Bullos"
/lab.hoft="Bullos"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/clone lib="Corgan: Pancreas; Vector: pBluescript SK(-); Site_I:
NotI; Site_2: XhoI; CDNA made by oligo-dT priming
Size-selected on agarces gel. Average insert size ~lkb. 5'
XhoI site was destroyed after directional cloning.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, Ermail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
/note="Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by Oligo-dT priming. Size-selected by column fractionation; average insert size 0.97 kb. Amplified once on solid support. cDNA Library Preparation: Guolin Chen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ270082 600 bp mRNA linear EST 15-JUL-2003 ik33902.yl HR85 islet Homo sapiens cDNA clone IMAGE:5782850 5' similar to SW:TRY2_HUMAN P07478 TRYPSINOGEN II PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Email: dmelton@biohp.harvard.edu
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Mashington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                              Length 577;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                              Score 26; DB 13; | Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                          2.4%; bcc...
100.0%; Pred. No. '...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 TGCCAGGGTGATTCTGGGGGCCCCCT 438
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High quality sequence stop: 422.
Location/Qualifiers
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/db_xref="taxon:9606"
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590 CCTGCCAGGGTGATTCTGGGGGCCC 614

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BI794700/c
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Note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Note_1: Site_2: Xho1; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. S;
Xho1 site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St.
louis, MO 53110, B-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-777-2692."
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Mashington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 636)
                                                                                                                                                                                                                                                                                           BQ269009
ik19g10.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5781690 5'
similar to SW:TRY2_HUMAN P07478 TRYPSINOGEN II PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melton, D. Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                    Gaps
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Other ESTs: ik19g10.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                  Length 600;
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/tissue_type="Purified pancreatic islet"
/lab_host="DH108"
                                                                    0; Indels
               DB 13; I
1.4e+03;
             2.3%; Score 25; DB
100.0%; Pred. No. 1.4
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: -40RP from Gibco
High quality sequence stop: 478.
Location/Qualifiers
                                                                                                                    CCTGCCAGGGTGATTCTGGGGGCCC 728
                                                                                                                                                                 566 ccreccadegrearrereeeeccc 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens (human)
Query Match
Best Local Similarity 100.C
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                                                                                                                                                                                                                                              RESULT 10
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Gaps

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0; Indels

2.3%; Score 25; DB 13; Length 636;

Pred. No. 1.3e+03;

100.0%; Pred. nc.

Conservative

Local Similarity es 25; Conserva

Best Loc Matches

Query Match

704 CCTGCCAGGGTGATTCTGGGGGCCC 728

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Note="Vector: pspoRT1; Site 1: Not I; Site_2: Sal I; Five libraries representing BIO.5/12.5 pancreatic bud, E16.5 pancreas, and adult pancreas, and adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaloo, Lennon, and Soares 1966 Genome Research 6:791-806; 0.5 microgram Single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (Unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Trace considered overall poor quality
MGI:1944668 This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E (Bases 1 to 283)

S Holton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other Ests: ic65e04.y2

Consect: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
BI794700
283 bp mRNA linear EST 12-MAR-2002 ic63e04.x2 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5658342 3' similar to SW:EL1_PIG P00772 ELASTASE 1 PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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/clone="1MAGE:5658342"
/sex="Both for embryonic & newborn, male for adult and adult islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
/lab host="DH10B"
/clone lib="Melton Normalized Mixed Mouse Pancreas 1
N1-MMSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 283
/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                              BI794700.1 GI:15822425
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Query Match Local

ORIGIN

Matches

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DEFINITION

RESULT 12 AI322408 LOCUS ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES

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Gaps

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EST 04-NOV-2002

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/organism="Homo sapiens"

/mol type="mRNA"

/mol type="mRNA"

/dob_xref="taxon:9606"

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/dob_pos="taxon:9606"

/lab host="Upe="Human lung Epithelial cells"

/lab host="Ul-Cr-FNO"

/lab host="Ul-Cr-FNO"

/clone lib="Ul-Cr-FNO"

/noce="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR i; Site 2: Not I;

Ul-Cr-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (ENI and DUI) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:

TAG_INSUB=Lung Epithelial Cells Tissue nos 359-368

TAG_LIB=UJ-CF-FNO

TAG_SEQ-GGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
The following repetitive elements were found in this cDNA
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo. I (bases 1 to 451)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                            451 bp mRNA linear EST 04-NV UI-CF-FN0-aey-o-05-0-UI.81 UI-CF-FN0 Homo sapiens CDNA clone UI-CF-FN0-aey-o-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCray Lab
University of Iowa
Uo24 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
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100.0%; Pred. No. 6.2e+03;
Live 0; Mismatches 0; Indels
   Indels
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0
   0; Mismatches
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Genome Res. 6 (9), 791-806 (1996)
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                                                                                                         147 GCTCCAGTGCCTCAACCTCTCCA 169
                                                                 594 GCTCCAGTGCCTCAACCTCTCCA 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA313295.1 GI:24531393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: McCray, PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
23; Conservative
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Best Local Similarity
Las 23; Conservat
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CA313295/c
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/mol type="mRNA"

/db_xref="txxxn:1009u"

/db_xref="txxxn:1009u"

/clone="txxxn:1009u"

/db_xref="txxn:1000u"

/clone="txxxn:1000u"

/db_host="hlu08 (ampicillin resistant)"

/clone lib="Scares mouse p3NMF19.5"

/clone lib="Scares mouse p3NMF19.5"

/clone lib="site="txxnunch"

/clone lib="site="txxnunch"

/clone lib="txxnunch"

/clone lib="txxnunch"

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/clone lib= "txxnunch"

/clone lib= "tx
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 449)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Ten,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 23-DEC-1998
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Putative full length read vector length is 607

Seq primer: -40RP from Gibco
High quality sequence stop: 408.
                                                                                                                                                                                                                                                                                                                                                                                                             mi20011.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:464085 5' similar to SW:TRY3_SALSA P35033 TRYPSINOGEN III PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                      ;
                                                      2.2%; Score 24; DB 12; Length 283; 100.0%; Pred. No. 4.5e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 23; DB 9; Le
100.0%; Pred. No. 6.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                    708 CCAGGGTGATTCTGGGGGCCCCCT 731
                                                                                                                                                                                                                                                    167 CCAGGGTGATTCTGGGGGCCCCCT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI322408.1 GI:4056837
                                                                                                                                   Conservative
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Best Local Similarity
                                                                                              Similarity
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Gaps

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ORIGIN

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SOURCE
ORGANISM
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AUTHORS
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JOURNAL
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX514743 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGP998N221098; IMAGE:464085, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                AA028356 506 bp mRNA linear EST 11-SEP-1996 mi20d11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:464085 5' similar to SW:TRYP_BOVIN P00760 TRYPSINOGEN ;, mRNA
                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 506)
Marram M., Hillier,L., Alllier,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra MyNouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 23; DB 9; Length 506; 100.0%; Pred. No. 5.7e+03; tive 0; Mismatches 0; Indels
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High quality sequence stop: 486.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX514743.1 GI:32244696
                                                                                                                                       AA028356
AA028356.1 GI:1494434
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BX514743
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VERSION
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                                     RESULT 14
                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                         AUTHORS
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                                                     AA028356
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                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 520)
Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: T7, Primer sequence: TAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPD; IMAGD998N221098.
RZPD; IMAGD998N221098.
RZPDIS (RZPDLIB NO.981)
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
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http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 101
Fax: +49 30 32639 111
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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/organism="Mus musculus"
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Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                             Mouse UnigeneSet - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                  and Korn, B.
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GenCore version 5.1.6
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using sw model protein search, OM protein June 16, 2004, 20:26:06; Search time 60 Seconds (without alignments) 1167.863 Million cell updates/sec Run on:

US-10-015-385A-194 1374 1 MGLSIFLLCVLGLSQAATP. Title: Perfect score:

Sequence:

.....GVYTYICKYVDWIRMIMRNN 248

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Winimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

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	ion	Human				_			Human	Novel	Human	_	Human		Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	
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SOUTHWILES	ΠD	AAB21304	AAB24428	AAB24032	AAY99393	AAM23994	AAB66142	AB033635	AB044488	AB033512	ADC18063	ADD70709	ADD39786	ADD70232	ADD38353	ADD39309	ADD38832	ADD40263	ADE50484	ADE20096	ADE50007	ADE21565	AA 029516	AAB21303	ABG66676	
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æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.5	94.7	94.7	
	Score	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1374	1367	1301	1301	1
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Aay28642 Aay32852 Aay41744 Aay40320 Aab21322 Aab44300 Aay12369 Aau12369 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852 Abb84852	Abu84932
AAY28642 AAY32852 AAY41744 AAY41744 AAY41322 AAB21322 AAB21332 AAB233087 AAB33087 AAB33373 ABB84852 AAB94853 ABB95458 ABB95458 ABB95458 ABB95458 ABU7255246 ABU7225246 ABU72252	ABU84932
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811 633 633 633 633 633 633 633 633 633 6	630.5
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45

ALIGNMENTS

Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; kallikrein-like protein; serine protease; cytostatic; cancer; AAB21304 standard; protein; 248 AA. (first entry) Human KLK-L5 protein #4. prostrate cancer. WO200053776-A2. Homo sapiens. 02-FEB-2001 14-SEP-2000. AAB21304; RESULT 1 AAB21304

09-MAR-2000; 2000WO-CA000258.

99US-0124260P. 99US-0127386P. 99US-0144919P. 11-MAR-1999; 01-APR-1999; 21-JUL-1999;

(MOUN) MOUNT SINAI HOSPITAL

Diamandis EP; Yousef GM,

WPI; 2000-587440/55. N-PSDB; AAA95944.

New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.

Claim 12; Page 172; 184pp; English.

The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KLK-L4 gene. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent bloological activity. Nucleic acids encoding Kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-M nuclein solated. The proteins are useful in the treatment. They monitoring and diagnosis of cancers, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used

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The present invention describes mucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and disquosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA7721 and AAB24188 to AAB24415 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ISNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVTYICKYVDW 240
                                                                                                       Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
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                Paoni NF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 248;
Hillan KJ;
Kuo SS, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1374; DB 3;
100.0%; Pred. No. 3.8e-98;
ive 0; Mismatches 0;
Gerber H,
Klein RD,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO1303 protein sequence SEQ ID NO:33
, Ferrara N,
I, Gurney AL,
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB24032 standard; protein; 248 AA
                                                                                                                                                                           Claim 72; Fig 82; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 248; Conservative
Ashkenazi AJ, Baker KP,
Goddard A, Godowski PJ,
Smith V, Watanabe CK, V
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                                                             WPI; 2000-412154/35.
N-PSDB; AAA77671.
                                                                                                                                                                                                                                                                                                                                                                                                                present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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                                                                                             Gaps
                                                                                             ;
0
                                                              Length 248;
   conditions mediated by the kallikrein-like proteins
                                                                                             Indels
                                                             100.0%; Score 1374; DB 3;
100.0%; Pred. No. 3.8e-98;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO1303 protein sequence SEQ ID NO:203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB24428 standard; protein; 248 AA
                                                                 100.08; Fr.
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99WO-US021547.
99WO-US023089.
99US-0162506P.
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99US-0141037P.
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                                                                                             Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 IRMIMRNN 248
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                                                                             Local Similarity
                                Sequence 248 AA;
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16-DEC-1999;
12-DAN-1999;
12-MAR-1999;
12-MAR-1999;
14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
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    to treat
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05-OCT-1
                                                                Query Match
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Gaps

9 9 240

120 120

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Human, PRO polypeptide, membrane bound protein, receptor, diagnosis, transmembrane, secretion, immunoadhesion, pharmaceutical, screening.
           Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0100664P
98US-0100684P
98US-0100644P
98US-0100711P
98US-0100919P
98US-0100910P
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9805-0100388P.
9805-0100390P.
9805-0100584P.
9805-01006627P.
9805-0100661P.
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9805-0101071P-
9805-0101471P-
9805-0101472P-
9805-0101474P-
9805-0101476P-
9805-0101476P-
9805-0101476P-
9805-0101478P-
9805-0101738P-
9805-0101738P-
9805-0101738P-
9805-0101741P-
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98US-0101916P.
98US-0102207P.
98US-0102240P.
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98US-0102330P.
98US-0102331P.
98US-0102484P.
98US-0102487P.
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98US-0099754P.
98US-0099763P.
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98US-0098843P.
98US-0099536P.
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98US-0099808P.
98US-0099812P.
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98US-0099642P
                                                                                                                                                   99WO-US020111
                                                                                                WO200012708-A2.
                                                                         Homo sapiens.
                                                                                                                                                   01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                           .0-SEP-1998
                                                                                                                         09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6-SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7-SEP-
3
                                                                                                                                                                                                                                                                        The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO4367; PRO1925; PRO1293; PRO1303; PRO4344; PRO4344; PRO4344; PRO4344; PRO43440; PRO1555; PRO1096; PRO2038; and PRO2266. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells.

Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonuclectide which hybridises to genes encoding (I). can be used to inhibit the present invention can be used to inducing (I). can be used to inhibit the biological activity of (I). AAC58019 conducing cell death. Methods from the present invention can be used to inducing cell death. Methods from the present invention for human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA 60
                                                                                                                                                                                                  Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                       Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccn 100.0%; Score 1374; DB 3; Length 248; al Similarity 100.0%; Pred. No. 3.8e-98; 248; Conservative 0; Mismarchin
                                                                                                                                       Roy MA, Watanabe CK,
                                                                                                                                          Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY99393 standard; protein; 248 AA.
                                                                                                                                                                                                                                                     Claim 61; Fig 24; 226pp; English.
                                   99WO-US005028.
99WO-US020111.
99US-0162506P.
99WO-US028313.
              99WO-US028551
                                                                                        99WO-US028634
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                                                                                                                                        Goddard A,
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                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                WPI; 2000-594320/56.
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Best Local Similarity
                                                                                                                                                                              N-PSDB; AAC58114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2000
                                                 01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
              02-DEC-1999;
                                                                                      01-DEC-1999;
                                                                                                                                          3otstein D,
                                       08-MAR-1999;
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Gaps

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120

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Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                          AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
                                                                                                                                                                                                                                                                                                                                                                    61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
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    receptor/ligand interactions
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                                                                                                                                                                                                                                          Length 248;
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100.0%; Score 1374; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0;
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Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human EST encoded protein SEQ ID NO: 1519
    of the relevant
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                                 Claim 12; Fig 108; 773pp; English.
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17-JUL-2000; 2000US-0061746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
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   molecule inhibitors
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98US-0105882P.
98US-0106062P.
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98US-0106856P.
98US-0106902P.
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98US-0103315P.
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17-NOV-1998;
17-NOV-1998;
17-NOV-1998;
17-NOV-1998;
18-NOV-1998;
               01-0CT-1998
01-0CT-1998
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08-0CT-1998
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27-0CT-1998;
27-0CT-1998;
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28-0CT-1998;
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obesity; auditory hair cell regeneration; hearing loss; bone disorder;
05-JAN-2000; 2000WO-US000219.
                                    (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                    Sequence 248 AA;
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                                                                                                                   proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
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                                                                                                         The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                             1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
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                                                                                                                                                                                                                                                                                                                                                                                                                            TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                                           Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                 Gaps
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                                                                               20; Page 1048-1049; 1275pp; English.
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99US-0144758P.
99US-0145698P.
99WO-US020111.
99US-0162506P.
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Best Local Similarity 100.
Matches 248; Conservative
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     WPI; 2001-476164/51.
N-PSDB; AAH98653.
                                                                                                                                                                                                                           Sequence 248 AA;
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29-OCT-1999;
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                                                                               Claim
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                                                                                   Watanabe CK;
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                          Fong S;
Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                             These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nuclasmay also be used in gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
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                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to secreted and transmembrane proteins
                                                                                                                                                                                                               Secreted and transmembrane proteins and nucleic acids designated
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                                               Gurney AL,
A, Tumas D,
                       Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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DONEL AR, Botstein D, Desnoyers L, Eaton DL, Fe
Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gu
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA,
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1374; DB 4;
Pred. No. 3.8e-98;
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                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 108; 787pp; English.
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100.0%; Pr
tive 0;
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98US-0103258P

98US-0103449P

98US-0103315P

98US-0103335P

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99US-0141037P.
99US-0144758P.
99WS-0145698P.
99WO-US020111.
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30-NOV-1999; 99WO-US028313
02-DEC-1999; 99WO-US028551
16-DEC-1999; 99WO-US030095
05-JAN-2000; 2000WO-US000219
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1-SEP-1999;
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       cartilage disorder; sports injury; arthritis.
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98US-0099741P.
98US-0099741P.
98US-009972P.
98US-009981SP.
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98US-0098723P.
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98US-0098813P.
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01-OCT-1998;
02-OCT-1998;
                                                        Homo sapiens.
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18-SEP-1998
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antidiabetic; anorectic, antiarthritic; angiogenesis; cancer; adrenal cortical capillary, endothelial cell growth; wound healing; stimulated T-lymphocyte proliferation; immune response suppression; neonatal heart hypertrophy; cardiac insufficiency disorder; vascular endothelial growth factor; inflammation; monounclear cell; eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia; chondrocyte redifferentiation; bone disorder; cartilage disorder; sports injury; arthritis.
                                                                                                                                                                                                                                                 98US-0098723P

98US-0098723P

98US-0098821P

98US-0098821P

98US-0099536P

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98US-01
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                                                                                                                                 Homo sapiens.
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02-SEP-1998;
09-SEP-1998;
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               , Fong S;
Hillan KJ;
, Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 that modulate glucose or free fatty acid uptake by skeletal muscle cells, and are useful for treating diabetes, hyper- or hypo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLIRLRLPVRV
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                                                                                                                                                                                                                                                                                                                                               Ferrara N,
                                                                                                                                                                                                                                                                                                                                           Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;
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                                                                                                                                                                                                                                  2001WO-US017800.
; 2001WO-US019692.
; 2001WO-US021066.
; 2001WO-US021735.
                                                               2000WO-US005841.
2000WO-US006884.
2000WO-US013705.
2000WO-US014042.
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2000WO-US030873.
2000WO-US032678.
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2001WO-US006666.
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2000WO-US004342.
2000WO-US005004.
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N-PSDB; ACD68378.
                                                              02-MAR-2000;
15-MAR-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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24-AUG-2000;
08-NOV-2000;
10-NOV-2000;
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28-FEB-2001;
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98US-0114223P.
99WO-US000106.
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99US-0141037P.
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05-JAN-1999
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Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S; Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK; Williams PM, Wood WI;
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Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0;
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   Human, secreted and transmembrane protein; PRO; gene therapy; vaccine; tissue typing; chromosome identification; vaccine.
                                                                                          Novel human secreted and transmembrane protein PRO1303
 ABO33512 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                      98US-0098716P.
98US-009873P.
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181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
                                                                                                                                                                                                                                      gene mapping;
                                                                                                                                                                                                                             Human; PRO; protein electrophoresis; chromosome mapping; genetic disorder.
                                                                                                                          ADC18063 standard; protein; 248 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1374; DB 7; Length 248; Best Local Similarity 100.0%; Pred. No. 3.8e-98; Matches 248; Conservative 0; Mismatches 0; Indels 0;
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01-MAR-2001, 2001WO-US006666.
01-JUN-2001, 2001WS-00872035.
01-JUN-2001, 2001WS-US017800.
14-JUN-2001, 2001WG-US019692.
20-JUN-2001, 2001WO-US019692.
29-JUN-2001, 2001WO-US01966.
              99US-0129674F
99US-0141037P
99US-0144758P
99US-0145698P
99WO-US020111
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2000WO-US003565.
2000WO-US004342.
2000WO-US005004.
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99WO-US028313.
99WO-US028551.
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2000WO-US013705.
2000WO-US014042.
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2000WO-US023522.
2000WO-US023328.
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N-PSDB; ACD68024.
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24-FEB-2000; 2
02-MAR-2000; 2
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17-MAY-2000; 2
22-MAY-2000; 2
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02-JUN-2000; 2
23-MUG-2000; 2
24-AUG-2000; 2
08-NOV-2000; 2
01-DEC-2000; 2
12-APR-1999;
16-APR-1999;
23-UUL-1999;
26-UUL-1999;
01-SEP-1999;
18-OCT-1999;
30-NOV-1999;
16-DEC-1999;
16-DEC-1999;
05-DAN-2000;
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211-FEB-2000;
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99WO-US021194 99WO-US021194 99WO-US028513 99WO-US0285513 99WO-US028551 200WO-US00035 2000WO-US00376 2000WO-US00376 2000WO-US00376 2000WO-US003765

2000WO-US014941. 2000WO-US015264. 2000WO-US023522.

2000WO-US023328 2000WO-US030952 2000WO-US030873 2000WO-US032678

2000WO-US013705. 2000WO-US014042.

us-10-015-385a-194.rag

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61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV 120
  18-NOV-1998;
18-NOV-1998;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.
                                                                                                                                                                                                                                                                                                              Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S; Gao W, Goddard A, Godowski PJ, Grimaldi UC, Gurney AL, Hillan KJ; Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe (Williams PM, Wood WI;
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100.0%; Pred. No. 3.8e-98;
ive 0; Mismatches 0;
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2001WO-US006520.
2001WO-US006666.
2001WO-US017800.
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2001WO-US021066.
2001WO-US021735.
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Matches 248; Conservative
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N-PSDB; ADC18062.
28-FEB-2001;
01-MAR-2001;
01-JUN-2001;
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Indels

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MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA

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31-100-1998;
31-100-1998;
31-100-1998;
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27-0CT-1998;
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   Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; cardium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLALALALPVRV
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                                                                     TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                               TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                  Human secreted/transmembrane protein PRO1303
                                                                                                                                                                           ADD70709 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                98US-0098716P.
98US-0098733P.
98US-0098732P.
98US-0098750P.
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98US-0099871P.
98US-009956R.
98US-009956R.
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98US-0100388P.
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98US-010054P.
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Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothbelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schoniain-Henoch purpura; coellac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
                                                                                                     61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
                                                                                                                                                                                           1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLJDHRWVLTA
                                                                  1 MGLSIFLLLCVLGLSQATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                        AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
                                                                                                                                     TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                  121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                       Gaps
                       0
   Length 248;
                       Indels
100.0%; Score 1374; DB 7;
100.0%; Pred. No. 3.8e-98;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                         ADD39786 standard; protein; 248 AA.
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2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004342.
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2000WO-US030952.
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2000WO-US032678.
2001WO-US006520.
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2000WO-US014941.
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2000WO-US013705
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Query Match
Best Local Similarity 100.
Matches 248; Conservative
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11-FEB-2000;
18-FEB-2000;
24-FEB-2000;
24-MAR-2000;
15-MAR-2000;
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15-SEP-1999;
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16-DEC-1999;
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Hillan KJ;
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A, Tumas D,
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Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gur
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA,
Williams PM, Wood WI;
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 98US-0107783P.
98US-0108775P.
98US-0108778P.
98US-010878RP.
98US-0108802P.
98US-0108802P.
98US-0108867P.
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2000WO-US014941.
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2001WO-US021066.
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99WO-US028313.
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2000WO-US030873.
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N-PSDB; ADD70708.
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16-APR-1999;
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181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
                                                                                                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane protein PRO1303.
                                                                                                                                                                                                                                           ADD70232 standard; protein; 248 AA.
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98US-0100385P.
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                                                                                                                                                                                                                                                                                        ADD70232;
                                                                                                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                                 The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to a maino acid sequence chosen from 123 fully defined sequences as sequence chosen from 123 fully defined sequences as second and acid sequences as encoding PRO, a vector comprising the PRO NA, a constraint call comprising the PRO NA, a constraint protein the vector producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-protein protein probe antibody. Pro is useful as molecular weight markers for protein clectrophoresis and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO NA are useful as hybridisation probes for a cDNA library to isolate the full-length PRO CDNA, PRO NA is useful for generating transgenic animals or knock-out animals which are useful for generating transgenic animals or knock-out animals which are useful for treating cransgenic animals or knock-out animals which are useful for treating cancerous tumours. PRO1260, PRO1410 polypeptides are useful for superpressing immune response. PRO1410 polypeptide are useful for treating cardiac insufficiency disorders. PRO1266 polypeptide are useful for treating cardiac insufficiency disorders. PRO1266 polypeptide are useful for treating benouse. PRO1275 and PRO1418 polypeptides are useful for treating benoments. PRO1275 and pRO1418 polypeptides are useful for treating benoment in skeletal muscle cells and obsenty. PRO1265, PRO1244 and PRO1382 polypeptides are useful for treating benomenting the present correct proper processents are useful for treating benoment in skeletal muscle cells and obsenty. PRO1265, PRO1245 pro1304, PRO1365, PRO1304, PRO1304, PRO1304, PRO1304, PRO1265, PRO1412, PRO1304, PRO1306, PRO1418, PRO1418, PRO1418, PRO1418, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419,
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Hillan KJ;
, Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                  New secreted and transmembrane PRO polypeptides useful for treating cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or hypo-insulinemia, sports injuries and arthritis.
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                                                                                                                                                                                                           Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; SEQ ID NO 194; 557pp; English.
01-MAR-2001; 2001WO-US006666.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
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04-SEP-2001; 2001US~00946374
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Fong S;
Hillan KJ;
Watanabe CK;
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100.0%; Score 1374; DB 7;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0;
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Gao W, Goddard A, Godowski
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   AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLRLPVRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
                                                                                                                                     AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRV
                                                                    TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                         TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
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28-PEB-2001; 2001MO-US006520.

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Gao W, Goddard A, Godowski
Pan J, Paoni NF, Roy MA, S
Williams PM, Wood WI;
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(GETH) GENENTECH INC.

Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S; good W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK; Williams PM, Wood MI;

WPI; 2003-786999/74.

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TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
                                                                                                                                                                                                                                                                                                                                                            121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
                                                                                                                                                                                                                                      MGLSIFLILCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGCVLIDHRWVLTA
                                                                                                                                                                                                               1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                                                                                                   Gaps
                        Novel isolated PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                    The invention relates to an isolated PRO polypeptide (secreted or
                                                                                                                                                                                   .;
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                                                                                                                                                 Query Match 100.0%; Score 1374; DB 7; Length 248; Best Local Similarity 100.0%; Pred. No. 3.8e-98; Matches 248; Conservative 0; Mismatches 0; Indels 0
                                                                                         Claim 12; SEQ ID NO 194; 550pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IRMIMRNN 248
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N-PSDB; ADD39308.
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RX FF FF X S X S S S S S
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Search completed: June 16, 2004, 20:32:43 Job time : 63 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 16, 2004, 20:30:31; Search time 20 Seconds (without alignments) 1192.775 Million cell updates/sec US-10-015-385A-194
1374
1 MGLSIFLLLCVLGLSQAATP......GVYTYICKYVDWIRMIMRNN 248 Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	neuropsin - mouse	trypsin (EC 3.4.21	(EC	EC CEC	trypsin (EC 3.4.21	serine proteinase	trypsin (EC 3.4.21	(EC	\sim	(EC 3.4.	\sim	\sim	trypsin (EC 3.4.21	~		trypsin (EC 3.4.21	tissue kallikrein		tissue kallikrein		trypsin (EC 3.4.21	kallik	trypsin (EC 3.4.21	tissue kallikrein		a)	_	(EC	27
SUMMAKIES	ID	I56559	855066	S55067	TRPGTR	A35871	A53968	B25528	TRBOTR	S13813	TRDG	TRDGC	A27547	TRRT1	831779	805494	TRRIZ	A31136	KQPG	A25606	JQ1471	JQ1472	A34079	S31778	A27207	S45303	NGMSG	7	17	A37938
	DB																				7									
	Query Match Length	260	248	248	231	243	253	246	229	247	247	246	247	246	238	247	246	261	232	261	246	246	261	231	239	261	261	242	242	260
ok	Query Match	45.3	41.4	41.3	40.8	40.4			ö	40.0	e,	φ.	φ.	39.5	φ,	æ.	38.7	æ,	38.1	•	•	37.7	37.7	37.4	٠	•	37.2	•	37.0	
	Score	622.5	9	267	261	555	555	553	552	550	546	545	544.5	543	540	533.5	532	527.5	524	520.5	519	518	518	513.5	13.	11.	10.	208	0	0
	Result No.	1	7	ť	4	S	φ	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

tissue kallikrein	tissue kallikrein	trypsin (EC 3.4.21	trypsin (EC 3.4.21	tissue kallikrein	trypsin (EC 3.4.21	tissue kallikrein	tissue kallikrein	trypsin (EC 3.4.21	tissue kallikrein	trypsin (EC 3.4.21	78 nerve growth fa	trypsin (EC 3.4.21	tissue kallikrein	tissue kallikrein	tissue kallikrein
S15686	B31136	B25852	S3904B	TRMSMS	S494B9	833772	S01971	A25852	KQHU	S39047	NGMSA	TRDFS	A41020	A44284	JE0236
~	N		N	Н	ď	N	0	Н	Н	N	Н	Н	~	N	7
263	259	247	241	261	242	257	261	247	262	240	256	229	261	244	261
36.6	36.5	36.5	36.4	36.1	36.1	36.1	36.1	36.0	35.9	35.8	35.7	35.7	35.7	35.6	35.3
33	502	501	499.5	5.96	496	495.5	495.5	494.5	493	491.5	491	490.5	490.5	489	485.5
503			4	4		•	-								

ALIGNMENTS

RESULT 1 IS6559

neuropsin - mouse C;Species: Wis musculus (house mouse) C;Date: 26-Unl-1996 #sequence_revision 26-Unl-1996 #text_change 21-Unl-2000 C;Date: 26-Unl-1996 #sequence_revision 26-Unl-1996 #text_change 21-Unl-2000 C;Accession: I56559 R;Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Ni J. Neurosci. 15, 5088-5097, 1995 A;Itle: Expression and activity-dependent changes of a novel limbic-serine protease A;Reference number: I56559; MUID:95348917; PMID:7623137 A;Reterence number: I56559; MUID:95348917; PMID:7623137 A;Reterence preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Reterences: GB:D30785; NID:g1648847; PIDN:BAA06451.1; PID:g1020091 C;Superfamily: trypsin; trypsin homology F;33-252/Domain: trypsin homology <try></try>	Query Match Query Match Best Local Similarity 49.0%; Pred. No. 1.4e-43; Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;	QY 5 IFILLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWYLTAA 61	QY 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLIRLPVRV 120
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RESULT 2
S55066
Lrypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
Lrypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N.Alternate names: trypsingen II
C;Species: Gallus gallus (chicken)
C;Bate: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
C;Accession: S55066; S72347
R;Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995

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A;Reference number: S71155
A;Accession: S71155
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ses 115; Conserv
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 28-005-1996 #sequence revision 07-Feb-1997 #text_change 21-Jul-2000
C;Accession: S55067; S72245; S55065; S72346; S71155
R;Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479; 1995
A;Title: Isolation and characterization of the chicken trypsinogen gene family.
A;Reference number: S55065; WUID:95251611; PMID:7733885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                        A.Molecule type: DNA
A.Residues: 1-248 cWAN2>
A.Residues: 1-248 cWAN2>
A.Residues: 1-248 cWAN2>
A.Residues: 1-248 cWAN2>
A.Experimental source: clone 2-229
C.Superfamily: trypsin; trypsin howology
C.Superfamily: trypsin; trypsin howology
C.Superfamily: trypsin; trypsin periodic and agentic protein serior profiles: pydrolase; protein digestion; serine proteinase; zymogen F.1-16/Domain: signal sequence #status predicted <SIG>
F.17-25/Domain: activation peptide #status predicted <APT>
F.26-24/Domain: trypsin II #status predicted <WAT>
F.26-24/Domain: trypsin homology <TRX>
F.56-241/Domain: trypsin homology <TRX>
F.56-109,202/Active site: His, Asp, Ser #status predicted
60 AAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRIRLPVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 AAHCYKSRIQVRLGEXNIDVQEDSEVVRSSSVIIRHPKY--SSITLNNDIMLIKLASAVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 ITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 VISSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:9603903
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Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN3>
Cross-references: EMBL:U15155, NID:g603902; PIDN:AAA79912.1; PID:g
Experimental source: clone Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:U15155; NID:g603902; PIDN:AAA79912.1; PID:gA;Experimental source: clone Pl
A,Accession: $72346
A,Molecule type: DNA
A,Nolecule type: DNA
A,Residues: 1-9, 'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.4%; Score 569.5; DB 2; Length; 47.5%; Pred. No. 2.9e-39; tive 39; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
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A;Molecule type: mRNA
A;Residues: 1-248 < WML1.
A;Cross-references: EMBL;U15156; NID:g603904
A;Experimental source: clone 1-P38
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Residues: 1-248 <WAN2>
Experimental source: clone 1-P38
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A, Molecule type: DNA
A, Residues: 1-248 <W
A, Experimental source
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A;Residues: 1-10 cCHA>
R;Hermodson, M.A.; Bricsson, L.H.; Neurath, H.; Walsh, K.A.
Biochemistry 12, 3146-3153, 1973
A;Title: Determination of the amino acid sequence of porcine trypsin by sequenator A;Reference number: A90368; MUID:73258692; PMID:4738933
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C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin pancreas, polymorphism; protein digestion; serine proteinas
F; 1-31/Product: trypsinogen #status experimental <ZYM>
F; 1-8/Domain: activation peptide #status experimental <APT>
F; 9-224/Domain: trypsin #status experimental <MAT>
F; 9-224/Domain: trypsin homology <TRY>
F; 9-224/Domain: trypsin homology <TRY>
F; 15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted
F; 48,92,185/Active site: His, Asp, Ser #status predicted
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C;Species: Sus scrota domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A9641; A90388; A00947
R;Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.
Biochim. Biophya. Acta 69, 115-129, 1963
A;Title: Su le trypsinogene et la trypsine de porc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 PGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
A;Cross-references: GB:U15155; NID:g603902; PIDN:AAA79912.1; PID:g603903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.3%; Score 567; DB 2; ilarity 45.5%; Pred. No. 4.6e-39; Conservative 38; Mismatches 88;
                                                  A,Experimental source: clone Pl
R,Mang, K.
submitted to the EMBL Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 KYVDWIRMIMRNN 248
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National proteinase SCCE precursor - human
National Stratum corneum chymotryptic enzyme
C.Species: Homo sapiens (man)
C.Date: 07-Unl-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C.Accession: A53968
R.Hansson, L.; Stroemgrist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud
A; Hitle: Cloning, expression, and characterization of stratum corneum chymotryptic e
A; Reference number: A53968; MUD: 94308225; PMID: 8034709
A; Actus: preliminary
A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Cross-references: GB: L33404; NID: 9521214; PIDN: AAC37551.1; PID: 9532504
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A; Residues: 1-246 cSTE>
A; Cross-references: GB: X04574; NID: 954918; PIDN: CAA28243.1; PID: 954919
A; Cross-references: GB: X04574; NID: 954918; PIDN: CAA28243.1; PID: 954919
C; Superfamily: trypsin, trypsin homology
C; Keywords: calcium binding; bydrolase; protein digestion; serine proteinase
F; 1-24-246 (Product: trypsin #status predicted cMAT>
F; 24-246 (Product: trypsin #status predicted cMAT>
F; 24-239 (Domain: trypsin homology cTRY>
F; 24-239 (Domain: trypsin homology cTRY>
F; 24-239 (Domain: trypsin homology cTRY>
F; 24-231 (100, 200, Active site: His, Asp, Ser #status predicted
F; 31.07, 200, Active site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trypsin (EC 3.4.21.4) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Decies: O-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C;Accession: B25528
R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARSILLPLOILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQVALLSGNQLHCGGVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 DHRWYLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NERWYLTAAHCKMNEYTVHLGSDTLG--DRRAQRIKASKSFRHPGY--STQTHVNDLMLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 HGVYPGRITSNMVCAGGVPG--QDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 TKVYKDLLENSMLCA-GIPDSKKNACNGDSGGPLVCKGTLQGLVSWGTF-PCGQPNDPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 RIRLEVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGLSIFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Sequence organisation and transcriptional regulation of A,Reference number: A93646; MUID:87066713; PMID:3641189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 246
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40.2%; Score 553; DB 2;
Best Local Similarity 44.7%; Pred. No. 6.3e-38;
Matches 113; Conservative 45; Mismatches 81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
40.4%; Score 555; DB 2;
Best Local Similarity 44.6%; Pred. No. 4.5e-38;
Matches 115; Conservative 37; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 7q35-7q35
C,Superfamily: trypsin; trypsin homology
F,30-245/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTYICKYVDWIRMIMRNN 248
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                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: B25528
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P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Xenopus lacvis (African clawed frog)
C;Species: Xenopus lacvis (African clawed frog)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 04-Mar-2000
C;Accession: A35871, 512117
R;Shi, Y.B.; Brown, D.D.
R;Shi, Y.B.; Brown, D.D.
R;Shi, Y.B.; Brown, D.D.
A;Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in A;Reference number: A35871; MUID:91007255; PMID:2210372
A;Gravic .....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS 122
                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                             HVSGWGITNHPRNPFPDLLOCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
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                                                                                                                                                                                                            99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 NMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI
                                                                                                                                                                                                            8 KIVGGYTCAANSIPYQVSLNSGSHF-CGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVL
                                                                                                                                                                                                                                                                    DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
predicted
                                                                                                                                                          21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: EMML:X53458; NID:g65162; PIDN:CAA37538.1; PID:g65163
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin protein disection are protein ase
E; 1-15, Domain: signal sequence #status predicted <SIG>F; 1-15, Domain: signal sequence #status predicted <APT>F; 1-20, Domain: activation peptide #status predicted <APT>F; 21-236, Domain: trypsin homology <TRY>F; 21-236, Domain: trypsin l #status predicted <AMT>F; 27-157, 45-61, 129-230, 136-233, 166-182/Disulfide bonds: #status predicted F; 60, 104, 197/Active site: His, Asp, Ser #status predicted
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glu) #status
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                                                        Length 231
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                                                                                                       Indels
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45.7%; Pred. No. 4.3e-38;
tive 42; Mismatches 82
                                               / Match 40.8%; Score 561; DB 1; Local Similarity 46.7%; Pred. No. 1.3e-38; nes 107; Conservative 39; Mismatches 77;
F;60,62,65,70/Binding site: calcium (Glu, Asn, Val,
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Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-243 <SHI>
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                                                        Query Match
                                                                                                             Matches
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mouse elastase

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7;

Gaps

81; Indels 14;

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us-10-015-385a-194.rpr

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C,Accession: A26273
R,Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. cell. Baiol. S, 2669-2676; 1986
Asyltile: Differential regulation of trypsinogen mRNA translation: full-length mRNA s A; Reference number: A26273; MUID:86284628; PMID:3841794
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                                     91 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC 140
                                                                                                                          141 HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lrypsin (EC 3.4.21.4) - bovine (cattle)
C;Species: Bos primiqenius taurus (cattle)
C;Species: Bos primiqenius taurus (cattle)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S;3813
R;le Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Bur. J. Biochem. 193, 767-773, 1990
A;Title: Isolation and nucleotide sequence of CDNA clone for bovine pancreat
A;Reference number: S;3813; MUID:91065383; PMID:1701147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.Alternate names: catîonic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 CYQYHIQVRLGEYNIDVLEGGEQFIDASKIIRHPKY--SSWTLDNDILLIKLSTPAVINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS
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                                                                                                                                                                                                                                                           200 SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
40.0%; Score 550; DB 2; Length 247;
Best Local Similarity 45.7%; Pred. No. 1.1e-37;
Matches 113; Conservative 40; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                     183 SGGPVÝCSGKLÓGIVSWGS--GCADKNKPGVÝTKVCNÝVSWÍKQTIASN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-247 <HUE>
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A; Molecule type: mRNA
A; Residues: 1-247 <PIN>
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A;Reference number: 800950; MUID;75146445; PMID:1092332

A;Contents: annotation; revisions

A;Note: the sequence agrees with that shown

R;Bode, W; Schwager. P.

J; Mol. 1910. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution

A;Reference number: A92594; MUID:76072097; PMID:512

A;Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Trypsinogen also occur after Arg-105.

C;Superfamily: trypsin; trypsin homology

C;Superfamily: trypsin peptide #status experimental <APT>

F;1-229/Product: trypsin homology

C;Superfamil: activation peptide #status experimental <APT>

F;1-225/Domain: activation peptide #status experimental <APT>
F;7-131,132-229/Product: alpha-trypsin #status experimental

F;6-7/Cleavage site: Lys-11e (enteropeptidase) #status experimental

F;13-143,31-47,115-216,122-189;14-416,303/Disulfide bonds: #status experimental

F;8,60,63,88/Binding site: Calcium (Glu, Asn, Val, Glu) #status experimental

F;131-132-(Leavage site: Lys-26) (autolytic) #status experimental
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C;Species: Bos primigenius taurus (cattle)
C;Accession: A90164; A00946; S08774
R;Mikes, O; Holeysovsky, V; Tomasek, V; Sorm, F.
Biochem: Biophys. Res. Commun. 24, 346-352, 1966
A;Title: Covalent structure of bovince trypeinogen. The position of the remaining A;Reference number: A90164; MUD:67168848; PMID:5967094
A;Molecule trype: protein
A;Molecule trype: protein
A;Residues: 1-57, 'Q',59-67, 'Q',69-150,'N',152-176,'N',178-229 cMIK>
R;Hartley, B.S.
Philos: Trans. R. Soc. Lond. B257, 77-87, 1970
A;Reference number: A93755
A;Contents: annotation; revisions
R;Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
B;Cohemistry 14, 1358-1366, 1975
                                                                                                                                                                                                                                                           119 RVISSVQPLPLPNDCATAGTECHVSGWG--ITNHPRNPFPDLLQCLNLSIVSHATCHGVY 176
                                                                                                                                                                                                                                                                                                                                                                                                                              21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL 80
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3 LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
                                 59 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV
                                                                                                                                                                   PGRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin (EC 3.4.21.4) precursor - bovine
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234 NYVDWIQNTIADN 246
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C;Accession: A51547
R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
Biochamistry, 26, 3081-3086, 1987
A;Fitle: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
A;Reference number: A27547; MUID:87271609; PMID:3607011
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-247 <FILE>
A;Cross-references: GB:MI6624; NID:g206498; FIDN:AAA41985.1; FID:g206499
C;Superfamily: trypsin, trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology <TRY>
F;25-240/Domain: trypsin homology <TRY>
F;31-164,196.55,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.J.; Rutter,
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #text_change 24-Sep-1999
C;Accession: B22657; A00948
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, J. Blol. Chem. 259, 14255-14264, 1984
A;Fille: Structure of two related rat pancreatic trypsin genes.
A;Fille: Structure of two related rat pancreatic trypsin genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 VRVTSSVQPLPLDPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYP
                                    119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG
                                                                                                              179 RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY
                                                                                                                                                              178 gissnimiciamegakbscogbsagevicnaelogivisma--acaokakpavspkycky
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                                                                                                                                                                                                                                                                                                                                                                                                                    - rat
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                                                                                                                                                                                                                         VDWIRMIMRNN 248
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A;Molecule type: DNA
A;Residues: 1-246 <CRA>
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A,Residues: 1-246 <PIN>
A,Molecule type: mRNA
A,Residues: 1-246 <PIN>
A,Cross references: GPIN>
A,Cross references: GPIN>
A,Cross references: GPIN>
C,Superfamily: trypsin; trypsin homology
C,Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <APT>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-246/Product: trypsin, cationic #status predicted <APT>
F;24-239/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;34-10,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;33,107,200/Active site: His, App, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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A;Cross-references: GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-23/Domain: trypsin, anionic #status predicted <ENZ>
F;24-23/Domain: trypsin homology <TRY>
F;34-160,48-64,132-233,139-206.171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLLCVLGLSQAATP----KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.7%; Score 545; DB 1; Length 246;
44.2%; Pred. No. 2.9e-37;
Live 43; Mismatches 87; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                        39.7%; Score 546; DB 1; Length 247; 45.6%; Pred. No. 2.4e-37;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 44.2
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.6'
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 IOSTIAAN 246
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80 73

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59 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
                                                                                                                                                                                                                                                       141 HVSGWGITNHPRNPFPDLLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD 199
                                                                                                                                                                                                                                                                                            132 LVSGWGNLSGSSSNYPDTLRCLDLPILSSSSCNSAYPGQITSNMFCAGFWEGGKDSCQGD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsin (EC 3.4.21.4) IV precursor - rat
NiAlternate names: 23K protein; trypsinogen IV precursor
C:Species: Rattus norvegicus (Norway rat)
C:Species: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
                                                                                                                                            81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
                                                                                                                                                                              SAAHCYKRKLQVRLGEHNIHVLEGGEQFIDAEKIIRHPEY--NKDTLDNDIMLIKLKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 VLNSQVSTVSLPRSCASTDAQCLVSGWGNTVSIGGKYPALLQCLEAPVLSASSCKKSYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 KIVGGYECRKNSASYQASLQSGYHF-CGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGLSIF--LLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKISIFFAFLGAAVALPVNDDDKIVGGYTCPKHLVPYQVSLHDGISHQCGGSLISDQWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY
                                       21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
                                                                                                                                                                                                                                                                                                                                                                                            SGGPVVCNGQLQGVVSWGY--GCAQRNKPGVYTKVCNYRSWISSTMSSN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S05494
R;Juetcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, Nucleic Acids Res. 17, 6736, 1989
A;Title: A fourth trypsinogen (P23) in the rat pancreas induced A;Reference number: S05494; MUID:89386010; PMID:2780302
                                                                                                                                                                                                                                                                                                                                                                SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
38.8%; Score 533.5; DB 2
Best Local Similarity 43.4%; Pred. No. 2.5e-36;
Matches 109; Conservative 41; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: June 16, 2004, 20:34:43
He : 21 secs
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                                       H
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A;Cross-references: GB:J000778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue
R;MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences
A;Reterance number: A00948; MUID:82265624; PMID:6896710
A;Accession: A00948
A;Molecule type: mRNA
A;Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S66657; S31779
EW: J. Biochem. 222, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of A;Reference number: S66657; MUID:96035908; PMID:7556223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
A, Residues: 1-238 <MAL>
A, Cross-references: EMBL: X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin; trypsin; trypsin; predicted <SIG>
C; Reywords: hydrolase; serine proteinase
F;1-7/Domain: signal sequence (fragment) #status predicted <ART>
F;1-238/Product: trypsin III #status predicted <ART>
F;16-231/Domain: trypsin homology <RRY>
F;16-231/Domain: trypsin homology <RRY>
F;16-231/Domain: trypsin homology SRX>
F;16-231/Domain: trypsin homology SRX>
F;16-231/Domain: trypsin homology SRX>
F;16-231/Domain: trypsin homology SRX>
F;2-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                               Ajintrons: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Superofamily: trypsin; trypsin homology
C;Superofa: hydrolase; pancteres; protein digestion; serine proteinase; zymogen
C;Keywords: hydrolase; pancteres; protein periode 4SIG>
F;16-23/Domain: signal sequence #status predicted <ADT>
F;24-23/Domain: activation peptide #status predicted <APT>
F;24-236/Product: trypsin nomology <ARX>
F;24-239/Domain: trypsin nomology <ARX>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGRITSNWVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSALLILALVGAAVÁFPLEDDDKÍVGGYTCPEHSVPYQVSLNSGYHF-CGGSLINDQWVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.5%; Score 543; DB 1;
44.5%; Pred. No. 4.1e-37;
live 47; Mismatches 76;
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Best Local Similarity 44.5%;
Matches 110; Conservative 4
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Best Local Similarity 47.2
Matches 108; Conservative
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Gaps

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June 16, 2004, 20:30:01; Search time 45 Seconds (without alignments) 1738.856 Million cell updates/sec
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1 MGLSIFILLCVLGLSQAATP......GVYTYICKYVDWIRMIMRNN 248
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                               1017041 segs, 315518202 residues
                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                              US-10-015-385A-194
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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:*

Database :

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:* sp_unclassified:* sp_virus:*
sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:*sp_phage:* sp_archeap:* sp_rodent:* sp plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9cv76 mus musculu	Q8iw69 homo sapien	Q8cgr4 mus musculu	Q8ixd7 homo sapien	Q9qyn4 mus musculu	Q9qym3 m hippostas	Q96rq0 homo sapien	Q9d140 mus musculu	Q8cgr6 mus musculu	Q8cgr5 mus musculu	Q80vs4 mus musculu	Q7sztl xenopus lae	Q7sz06 xenopus lae	O88301 mus musculu	Q91y82 mus musculu	Q9d7y7 mus musculu	
SUMMARIES	qı	Q9CV76	QBIW69	Q8CGR4	Q8IXD7	Q9QYN4	69QYN3	Q96RQ0	Q9D140	QBCGR6	QBCGR5	Q80VS4	Q7SZT1	Q7SZ06	088301	Q91Y82	Q9D7Y7	
	ı	H	4	11	4	11	11	4	11	11	11	11	13	13	11	11	11	
	* Query Match Length DB							255										
	% Query Match	69.3	45.7	44.3	43.7	43.5	43.5	43.3	42.8	42.8	42.6	42.1	41.0	40.4	40.3	40.3	40.1	
	Score	952.5	627.5	608	601	597.5	597.5	595	588.5	588	586	578	563	555	553.5	553.5	550.5	
	Result No.		7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	

Q9cpn9 mus musculu O54854 rattus norv Q8n5n9 homo sapien Q9cpn7 mus musculu	enu mus mus	eng ang pan rat	m ()	Q9w7q6 paralichthy Q8av11 oncorhynchu Q63274 rattus norv Q9w7q7 paralichthy Q42159 petromyzon	042160 petromyzon Q7sx90 brachydanio Q92046 dissostichu Q8iu55 homo sapien Q8tg9 engraulis j Q9w6k0 notothenia Q91515 fugu rubrip
Q9CPN9 O54854 Q8N5N9 Q9CPN7	091 VE3 09R0T7 07TT42 09Z1R9	098TH0 098TH0 07T1R8 063275	Q8AV83 Q9N1Q1 Q99M20 Q29474	Q9W7Q6 QBAV11 Q63274 Q9W7Q7 Q42159	042160 Q72X90 Q92X46 Q81U55 Q98TG9 Q9W6K0
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247 253 247	44444 44444	4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	243 261 278 278 261	23 2 2 2 2 3 4 4 2 4 4 4 4 4 4 4 4 4 4 4	2242 2442 2442 2442 2344 2344 7
39.00 39.00 39.60 4.00	38.00.08.00.00.00.00.00.00.00.00.00.00.00	38.2 37.4 4.7	3.7.E 4.7.E 4.7.E	37.2 37.1 37.1 37.0	36.5.3 36.5.3 36.5.4 5.5.5 5.5 5
549.5 546.5 541.5	533 533 533 533 533	525 525 522 514.5 514	513.5 513.5 513.5	510.5 509.5 509.5 508 508	506 505 504.5 504.5 503 502 502
113 119 20	2 2 2 2 4 5 4 5 4 5 5 5 5 5 5 5 5 5 5 5	7 7 7 8 7 8 7	10000 00000		W 44 44 44 44 44 44 73 14 15 15 15 15 15 15 15 15 15 15 15 15 15

01-JUN-2001 (TrEMBLrel. 17, Last Sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 2310008B01Rik protein (Fragment). 234 AA. (TrEMBLrel. 17, Created) PRT; PRELIMINARY; 01-JUN-2001 95V76 RESULT 1 95V76

ALIGNMENTS

Mus musculus (Mouse). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090; 2310008B01RIK.

REDURECE FROM N.A.

REDURECE TROM N.A.

REQUIRECE TROM N.A.

REQUIRECE TROM N.A.

REDURECE TO STANDER TO TISSUE TONGUE;

REDINES-1085660; DubMed-11217851;

REDUREL TO STANDER TO THE TONGUE;

RA ATARWAW T., HARA A., Shibhar K., Konno H., Adachi J., Fukuda S., RATAGAWA T., CARAWA T., RAWA A., RAWA A., Mishi K., Konno H., Adachi J., Fukuda S., Yamanaka I., RA Atawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rels Chmann W., Gasterland T., Gissi C., King B., Kochiwa H., Rachil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Rakai K., Okido T., Furubl R., Parsh G., Rashin J., Boffelli D., Bojunga N., Anno H., Baldarelli R., Barsh G., RA Shai K., Okido T., Furubn M., Anno H., Baldarelli R., Barsh G., RA Stai K., Okido T., Furubn M., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ashstincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyono P., Narohima J., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Rayushizaki Y., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Rayashizaki Y., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming Y., Rayashizaki Y., Toyo-Oka K., Hasegawa Y., Kawaji H., Kohtsuki S., R. Warnand annotation of a full-length mouse cDNA collection.";

P. Warnander Ang. Safe A. Mang K.H., Menter M. M. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander Ang. Safe A. Marnander A. Marnander Ang. Safe A. Marnander A. Marnander Ang. Safe A. Marnander A. Marnander A. Marnander A. Marnander A. Marnander A.

Nature 409:685-690(2001). -!- SIMILARITY: BELCNGS TO PEPTIDASE FAMILY S1. EMBL; AK009217; BAB26143.1; -.

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Gaps

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61

180

240

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62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLRLPVRV 120
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                                                                                                                                                    5 IFLLL --- CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                                                                                                                                                            121 TSSVQPLPLPUDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 IFLLLCVLGLSQAAT -- PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                        Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.3%; Score 608; DB 11; Length 254;
49.0%; Pred. No. 1e-50;
tive 30; Mismatches 77; IndelB 2:
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Adams M., Mural R.;
Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY152434; AAN78422.1;
EMBL; AY152434; EMYR422.1;
R GO; GO:0004263; F:chymotrypsin activity; IEA.
R GO; GO:0004295; F:chymotrypsin activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000903; Cys Ser trypsin.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001214; Peptidase_S1A.
                                                                                      Indels
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PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SEQUENCE 254 AA; 28042 WW; AA9E38BEBDD01861 CRC64;
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Last annotation update)
                    45.7%; Score 627.5; DB 4; 50.2%; Pred. No. 1.4e-52; tive 24; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 299:305-311(2002)
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nes 124; Conservative
                 Query Match
Best Local Similarity 50.2%
Matches 123; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 EHSLTKLDWTEQLRHTTFSITHPSYQGAYQNHEHDLRLLRLNRPIHLTRAVRPVALPSSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 ATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VITGAMCHVSGWGITINKPWDPPPDRLOCINLSTVSNETCRAVFPGRVTENMLCAGGEAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLG
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 234;
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L Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC0400807; AAH40887.1; -

R GO; GO:0004285; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chypsin activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001354; Peptidase_S1.

InterPro; IPR001354; Peptidase_S1.

R InterPro; IPR001354; Peptidase_S1.

R PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Trypsin, 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
MEMOPS, SULUZO; ...
MEMOPS, MGI.1201.201. ...
MGD; MGI.1916761; 2310008B01Rik.
MGD; MGI.1916761; 2310008B01Rik.
MGD; MGI.1916761; 2310008B01Rik.
MGD; MGI.1916761; 2310008B01Rik.
MGD; MGI.0004263; F:chypgin activity; IEA.
MGC; GO:00065083; F:peptidase and peptidolysis; IEA.
MICHERPO; IPRO01254; Peptidase_SIA.
MICHERPO; IPRO01254; Peptidase_SIA.
MICHERPO; IPRO01314; Peptidase_SIA.
PRINTS; PRO0722; CHYMOTRYPSIN.
MEMORITE; PRO0722; CHYMOTRYPSIN.
MEMORITE; PRO0724; TRYPSIN DOM; 1.
MEMORITE; PRO0134; TRYPSIN DOM; 1.
MEMORITE; PRO0134; TRYPSIN HIS; 1.
MEMORITE; PRO0134; TRYPSIN HIS; 1.
MEMORITE; PRO0134; TRYPSIN HIS; 1.
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SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 AA; 25888 MW; 6D81E609EDD39110 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Protease; Serine protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
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60 AHCRKPHYVILLGEHNLEKTDGCEQRRAATESFPHPDFNNSLPNKDHRNDIMLVKMSSPV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 RITSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 NITDIMLCASVRKEGKDSCQGDSGGPLVCNGSLQGIISWGQ-DPCAVTRKPGVYTKVCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
Mitsul S., Yamagushi N.;
Mitsul S., Yamagushi N.;
"CDNA cloning of a novel brain serine protease, Hippostasin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO16255; BAA88825.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.;
to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                            243 SWGQ-DPCAITRKPGVYTKVCKYVDWIQETMKNN 275
215 SWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 AA.
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MGD; MGI:1929977; Prss20.
GO; GO:005576; C:extracellular; IDA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
                                                                                                                                                                                                                  Created)
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RRINTS; PR00722; CTWONTYPEIN.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
SEQUENCE 249 AA; 27604 MW; F9FF
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Matches 118; Conservative
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                                                                                                                                                                    PRELIMINARY;
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Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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Q9QYN4
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                                                                                                                                                                                                                    CHGVYPGRITSNMVCA---GGVPGDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIP 228
                       CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS 122
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
"Molecular cloning and expression of a variant form of hippostasin/Kukii in prostate.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO78780; BAC54105-1;
S. GO; GO:0004263; F:chymotrypsin activity; IEA.
R. GO; GO:0004295; F:chymotrypsin activity; IEA.
R. GO; GO:0004295; F:chymotropysis and peptidolysis; IEA.
R. InterPro; IPR001254; Peptidase.Sl.
R. InterPro; IPR001254; Peptidase.Sl.
R. InterPro; IPR001214; Peptidase.Sl.
R. InterPro; IPR001314; Peptidase.Sl.
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PRINTS, PR00722; CHYMOTRYPSIN.

SMART; SM00202; TTYP SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN JBS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

SEQUENCE 275 AA; 30165 WW; 257A42B28F40E2C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                        SVQPLPLPNDCATAGTECHVSGWGITNHPRNP
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MEDLINE=20499374; PubMed=11042159;
MEDLINE=20499374; PubMed=11042159;
Korninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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SEQUENCE FROM N.A.
STRANIE-STBL/G17 IISSUE=Tongue;
The FANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Tongue;

Arakawa T., Arahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kaya K., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagawa M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

Subaha Y., Condo T., Faraka Y., Shibata K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,
                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hippostasin prostate type (Adult male tongue cDNA, RIKEN full-length
enriched library, clone:23100415108 product:protease, serine, 20, full
insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310040F07 product:protease, serine, 20, full insert
                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J, IISSUE=Tongue;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Prostate;
MEDLINE=20525460; PubMed=11072088;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
Mitsui S., Otuing and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Yamaguchi N., Mitsui
Submitted (JUL-1998)
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118
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ESPANDALE FROM N.A.

SEMULALS FROM N.A.

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; PubMed=11076861;

WEDLINE=20530913; Parawa K., Tashiro B., Itahada A.,

WATAMANOR C., Indue K., Togawa Y., Izawa M., Ohara E., Watshirki M.,

WEDLINE-20530913; Parawa K., Tanawa M., Matsunia S., Kawai J.,

WATAMANOR T., Ishikawa T., Ozawa K., Tanawa M., Matsunia S., Kawai J.,

WELLIAR INTERNIAL INTERPRETATION OF THE MATSULIAR SEQUENCET.";

Genome Res. 10:1757-1771(2000)

REMBL; AROU9705; BAB26461.2; -.

DR REMBL; AROU9705; BAB26461.2; -.

DR MGD; MG1:1929977; Pres20.

DR MGD; MG1:1929977; Pres20.

DR MGD; MG1:1929977; Pres20.

DR InterPro; IPR009003; Cys Ser Ltypsin.

DR InterPro; IPR001244; Peptidase=51A.

DR InterPro; IPR001244; Peptidase=51A.

DR FALLY DEFALLY SET AND SET LTYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 NIIDIMLCASVRKEGKDSCQGDSGGFLVCNGSLQGIISWGQ-DPCAVIRKPGVYIKVCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGLSIFLILCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 MILRLIALALVTGHVGGET-RIIKĞYECRPHSQPWQVALFQKTRLLCGATLIAPKWLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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43.5%; Score 597.5; DB 11; Length 276;
Best Local Similarity 47.0%; Pred. No. 1.2e-49;
Matches 118; Conservative 33; Mismatches 95; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90BDC03A8AB178D6 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
FYGIOLASE; PYOTGEASE; SETIME PIOCEASE.
SEQUENCE 276 AA; 30753 MW; 90BDC03A
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MEDLINE=21226193; PubMed=11327827;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23B VDWIRMIMRNN 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 FNWIHEVMRNN
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296RQ0
1D 096RQ
AC 096RQ
DT 01-DD
DT 01-DD
DT 01-DD
DC Euke
OC Euke
OC Mamma
OX NCBI
RP 5EQU
RX MEDL
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Created)
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Best Local Similarity
                                                                                                                                                                                                         HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GVYPGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYT
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MEDLINE=2108566), PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
Takayama T.K., Carter C.A., Deng T.; "Activation of prostate-specific antigen precursor (pro-PSA) by prostin, a novel human prostatic serine protease identified by degenerate PCR.";
                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                             Query Match
43.3%; Score 595; DB 4; Length 255;
Best Local Similarity 46.5%; Pred. No. 1.9e-49;
Matches 119; Conservative 32; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                     00D5B79E14B9468F CRC64;
                                                                                                                         GO, GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                    Biochemistry 40:1679-1687(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY EMBL, AR3046; AAK62813.1; -.
MESCP, POO761; 1AN1.
MEROPS; SO1.081; -.
                                                                                                                                                                                                                                 PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS0240; TRYPSIN DOM; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 255 AA; 27986 MW; 00D5B7
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240 KVCHYLEWIRETMKRN 255
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01-JUN-2001 (TEMBLrel, 17, 01-JUN-2001 (TEMBLrel, 17, 01-JUN-2001 (TEMBLrel, 17, 01-JUN-2001)
                                                                                                                                                                                                                     Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01-OCT-2003 (TrEMBLE).
1110030019Rik protein.
1110030019RIK.
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake U., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 ATPKIFNGTECGRNSQPWQVGLFEG-TSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 SSSRIVNGSDCOKDAOPWOGALLLGPNKLYCGAVLISPOWLLTAAHCRKPVFRIRLGHHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 EGTRCMVSGWGTTSSSHNNFPKVLQCLNITVLSEERCKNSYPGQIDKTMFCAGDEEGRDS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Last annotation update)
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42.8%; Score 588.5; DB 11;
Best Local Similarity 47.2%; Pred. No. 9.5e-49;
Matches 110; Conservative 41; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AK003996; BAB23113.1; -.
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237
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Q80VS4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 DHRWVLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST--SHEHDLR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 HPKWVLTAAHCRKDGYTVHLGKHALGRVENGEQAMEVVRSIPHPEYQVTPTHLNHDHDIM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 LIRLRLPVRVTSSVQPLPL-PNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 IACLTLALSEGISRDYPKILNGTNGTSGFLPGGYTCLPHSQPWQAALLIRGRLLCGGVLV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LLCV-LGLSQAAT---PKIFNGTE-----CGRNSQPWQVGLFEGTSLRCGGVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 ATCHGVYPGRITSNWVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 BECRQVYPGKITANMLCAGTKEGGKDSCEGDSGGPLICNGKLYGIISWGDF-PCGQPNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Gaps
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"Organization and evolution of the glandular kallikrein locus in Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.8%; Score 588; DB 11; Length 276; 46.3%; Pred. No. 9.9e-49; tive 38; Mismatches 81; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Adams M., Mural R., ;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY152433; AAN78421.1; -.
                                                                                     SEQUENCE FROM N.A.
Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                          Pran; PF00089; Erypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
BRART; SM00020; Tryp SPC:
PROSITE; PS50240; TRVPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SEQUENCE 276 AA; 30360 WW; 33E189C67492FDCA CRC64;
                                                                                                                                                     EMBL, AYISS432; AAN78420.1; ANS. MGD, MGI:95292; Klk13.

GO; GO:0004253; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:000508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR009003; Cys. Exer Lrypsin.

InterPro; IPR001354; Peptidase S1.

InterPro; IPR001314; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
KLK14.
                        musculus.";
Biochem. Biophys. Res. Commun. 299:305-311(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 GVYTRVSKYLRWIREIIRN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVYTYICKYVDWIRMIMRN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.3%
Matches 120; Conservative
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Q8CGR5
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| MFLLLILQALAVALAQSQGDHKIIGGYRCVRNSQPWQVALQAGPGHRPLCGGVLLSDQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 PGIITSGMVCA-GVPEGGKDSCQGDSGGPLVCGGQLQGLVSWG-MERCAMPGYPGVYANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 VLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 PVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 PGRITSNMVCAGGVP--GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IFLLLCVL----GLSQA-ATPKIFNGTECGRNSQPWQVGLFEGTSLR--CGGVLIDHRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.6%; Score 586; DB 11; Length 250; Sest Local Similarity 47.2%; Pred. No. 1.4e-48; Aatches 120; Conservative 40; Mismatches 80; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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STRAIN=NMRI; TISSUE=Breast tumor;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BCO44756; AAH44756.1; -.
R GO; GO:0004263; F:chymotrypsin activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001254; Peptidase_SI.
R InterPro; IPR001254; Peptidase_SIA.
MGD, MGI:2447564; KIk14.

GO; GO:0004263; F:chypain activity; IEA.
GO; GO:0004295; F:chypain activity; IEA.
GO; GO:0004295; F:chypain activity; IEA.
GO; GO:0004295; F:chypain activity; IEA.
GO; GO:0004295; F:chypain activity; IEA.
InterPro; IPR001203; Cys Ser Lrypsin.
InterPro; IPR001214; Peptidase_SI.
InterPro; IPR001214; Peptidase_SIA.
Fam; PR00121; CHYMOTAYPSIN.
FAMRI; SM00122; TYPP SPC; I.
FROSITE; PS50240; TRYPSIN DOM; I.
FROSITE; PS00134; TRYPSIN DOM; I.
FROSITE; PS00134; TRYPSIN SER; I.
FROSITE; PS00135; TRYPSIN SER; I.
FROSITE; PS00135; TRYPSIN SER; I.
FROSITE; PS00135; TRYPSIN SER; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                F62FEBF2290FEBE8 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similar to kallikrein 14 (Fragment)
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PRINTS; PR00722; CHYMOTRYESIN.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
SRQUENCE 242 AA; 26059 MW; A3F8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 CKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNYHSWIQRTMQSN 250
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and mouse cDNA sequences.";
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alaschul S.F., Zeeberg B. Suetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Hang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brapleron M., Soares M.B., Bonaldo M.F., Carrinci P., Prange C.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carrinci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broak S.A., McEwan P.J., McKernan K.J., Mahark J.A., Ghubarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rache J., Helton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Anderstion and initial analysis of more than 15,000 full-length human
                            ů,
                                                                                                         138
                                                                                                                        ECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP--GQDAC 196
                                                                                                                                                                               133 PCRVSGWGIIASPIARYPTALQCVNVNIMSEQACHRAYPGIITSGMVCA-GVPEGGKDSC 191
                                                    78
                                                                               74
                                                                             KIIGGYRCVRNSQPWQVALQAGPGHRFLCGGVLLSDQWVITAAHCARPILHVALGKHNIR
                                                     21 KIFNGTECGRNSQPWQVGLFEGTSLR--CGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLS
                                                                                                         QLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGT
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                  QGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                  MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic and genomic tools for Xenopus research: The NIH Xenopus
                          8;
 Length 242;
                          75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056068; AAH56068.1; -
                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Score 578; DB 11;
Pred. No. 7.9e-48;
                          35; Mismatches
                                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                              PRT;
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 42.1%;
49.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA sequences."
 Query Match
Best Local Similarity 49.1%
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Trypsin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
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Astrausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano M.S., Peters G.J., Abramson R.D., Prange C.,

Raha S.S., Morban P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                       AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLPVRV 120
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                                                                                                                                                                                                                                           S WKFLVILVILGAAVAFEDDDKIVGGFTCAKNAVPYQVSLNAGYHF-CGGSLINSQWVVSA
                                                                                                                                                                                                                                                                                                                                                            64 AHCYKSRIQVRLGEHNIALNEGTEQFIDSQKVIKHPNY--NSRNLDNDIMLIKLSTTARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD
                                                                                                                                                                                                      3 LSIFLLLCVLGLSQA--ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ISSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                               Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                               8;
                                                                                     Length 248;
                                                                                                                                               Indels
                           1ED9D0D218702860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                               83;
                                                                                  41.0%; Score 563; DB 13;
45.0%; Pred. No. 2.3e-46;
live 46; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seque
01-OCT-2003 (TrEMBLrel. 25, Last annot
Hypothetical protein.
Xenopus laevis (African clawed frog).
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MEDLINE=22388257; PubMed=12477932;
                     26494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Dyn. 225:384-391(2002).
                                                                                                                                         Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 WIQSTISSN 248
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1
248 AA;
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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us-10-015-385a-194.rspt

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MEROPS; S01.236; ...
MGD; MGI.1343166; Pres18.
GO; GO:0004265; F:chymotrypsin activity; I
GO; GO:0008233; F:peptidase activity; IEA.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurosin (Protease, serine,
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.5%
Matches 107; Conservative
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238 QNILRN 243
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TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                           FLLLCVLGLSQAAT---PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                  3 FLILCVL-LGAAAAPDDDKIIGGATCAKSSVPYIVSLNSGYHF-CGGSLITNQWVVSAAH
                                                                                                                                                                                                                                                                                                                                                                                                                           61 CYKASIQVRLGEHNIALSEGTEQFISSSKVIRHSGY--NSYTLDNDIMLIKLSSPASLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 NNVCAGGVP-GODACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 NMICVGFMEGGKDSCÓGDSGGPVVCNGOLÓGVSWGY--GCAMRNYPGVYTKVCNYNAWI
                                                                                                                                                                                                                                                                 Gaps
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"The sequences of mouse serine protease gene expressed in brain.";
"The sequences of mouse serine protease gene expresses in the sequences of mouse serine protease gene expresses.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO15206; BELONGS TO PEPTIDASE FAMILY S1.
EMBL, ABO15206; BAA27895.1; -.
EMBL, Y18723; CAA77269.1; -.
EMBL, ABO32402; BAA84544.1; -.
HSSP; PO0763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB-Brain;
Matsui H., Takahashi T.;
Matsui H., Takahashi T.;
Whouse serine protease preferentially expressed in brain.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C; TISSUE-Skin;
where N., Dear T.N., Boehm T.;
"A novel sexine protease expressed in the hair follicle.";
submitted (FRB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    40.4%; Score 555; DB 13; Length 2
45.7%; Pred. No. 1.3e-45;
tive 42; Mismatches 82; Indels
                                                                                    Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054194; AAH54194.1; -.
Hypothetical protein.
SEQUENCE 243 AA; 25476 MW; C5B82B458B209F31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                       Local Similarity 45.74
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                                            SEQUENCE FROM N.A.
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                                                                      rissum=Whole;
                                                                                                                                                                                                                           Query Match
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitsui S., Yamaguchi N.; "cDNA cloning and characterization of mouse brain specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.3%; Score 553.5; DB 11; Length 246; 43.5%; Pred. No. 1.9e-45; tive 46; Mismatches 82; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AB008928; BAB55605.1; -.
EMBL; BC031119; AAH31119.1; -.
HSSP; P00761; 1AN1.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 PERMIT PRODORS; trypsin; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
SWART; SMO0202; CHYMOTRYPSIN.
PROSTITE; PS0040; TRYPSIN DOM; 1.
PROSTITE; PS00134; TRYPSIN HIS; 1.
PROSTITE; PS00135; TRYPSIN ER; 1.
HYDTOLABE; PROTEABE; SETIME protease.
SEQUENCE 246 AA; 27496 MW; E20C080087139B63 CRC64;
GO, GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IFA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR009003; Cys. Ser. Lrypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
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Last annotation update)
18).
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                                                                                                                                                                                                                                                                           7 LLLCVLGLSQAA----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                             11,
                                                                                                                                                                                               Query Match
40.3%; Score 553.5; DB 11; Length 253;
Best Local Similarity 43.5%; Pred. No. 2e-45;
Matches 107; Conservative 46; Mismatches 82; Indels 11;
GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro: IPR001254; Peptidase S1.

InterPro: IPR001314; Peptidase S1A.

Fram; PF00089; trypsin; 1.

PROSITE; PS00134; TRYPSIN; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN ER; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 253 AA; 28329 MW; CSEF9BC7EEF2FBC1 CRC64;
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Job time : 47 secs
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